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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 11:18:58 ; Search time 14164 Seconds
(without alignments)
11487.759 Million cell updates/sec

Title: US-10-800-256-1
 Perfect score: 3358
 Sequence: 1 acgggtagaagattcttgat.....cctaattctctatagaacc 3358

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su

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Database : GenEmbl.*
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8: gb_pl.*
9: gb_pr.*
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12: gb_sy.*
13: gb_un.*
14: gb_vl.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Query %			Length	DB	ID	Description		
	Score	Match	Time						
1	3353.2	99.9	15186	6	BD218398	6	BD218398	Newcastle	
2	3353.2	99.9	15186	6	AR492934	6	AR492934	Sequence	
3	3353.2	99.9	15186	6	AX008510	6	AX008510	Sequence	
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5	3353.2	99.9	15186	14	NDVY18998	14	NDVY18998	Newcastle	
6	3342	99.5	15186	14	AY225110	14	AY225110	Newcastle	
7	3308.4	98.5	15186	14	AF375823	14	AF375823	Newcastle	
8	3305.2	98.4	15186	14	AF309418	14	AF309418	Newcastle	
9	3284.2	97.7	3819	14	AY289002	14	AY289002	Newcastle	
10	3199.6	95.3	3825	6	A03663	6	A03663	Newcastle	
11	3196.4	95.2	3825	6	E01252	6	E01252	Synthetic D	
12	3190	95.0	4552	14	AY289000	14	AY289000	Newcastle	
13	2826.8	84.2	3825	14	NDVPHN	14	NDVPHN	Newcastle	
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16	2577.2	76.7	3922	14	AY288987	14	AY288987	Newcastle	
17	2577.2	76.7	15192	14	AY562998	14	AY562998	Newcastle	
18	2551.6	76.0	3819	14	AY288992	14	AY288992	Newcastle	
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29	2442.8	72.7	3819	14	AY288993	Newcastle
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41	1748.4	52.1	11896	14	AY626267	Newcastle
42	1741.8	51.9	4177	6	AR093362	Sequence
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ALIGNMENTS

RESULT 1	
BD218398	linear PAT 17-JUL-2003
LOCUS	Newcastle disease virus infectious clones, vaccines and diagnostic assays.
DEFINITION	
ACCESSION	BD218398
VERSION	BD218398.1 GI:33028168
KEYWORDS	JP 2002518012-A/157.
SOURCE	Newcastle disease virus
ORGANISM	Newcastle disease virus
REFERENCE	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.
AUTHORS	1 (bases 1 to 15186)
TITLE	Peeeters, B.P.H., Leeuw, O.S.D., Koch, G. and Gielkens, A.L.J. Newcastle disease virus infectious clones, vaccines and diagnostic assays
JOURNAL	Patent: JP 2002518012-A 157 25-JUN-2002; ID LELYSTAD INSTITUUT VOOR DIERHOUDERIJ EN DIERGEZONDHEID BV
COMMENT	OS Newcastle disease virus PN JP 2002518012-A/157 PD 25-JUN-2002 PP 17-JUN-1999 JP 2000554854 PR 19-JUN-1998 EP 98202054.7 PI BERNARDUS PETRUS HUBERTUS PEETERS, OLAV SVEN DE LEEUW, GUUS KOCH, PI ARNOUD LEONARD JOSEF GIELKENS PC C12N15/09,A61K39/17,A61K48/00,A61P31/12,C12N7/00,C12Q1/70, PC C12N15/00 CC /note='Nucleotide sequence of NDV strain La Sota' CC /note='Nucleotide sequence of NDV strain La Sota' CC /note='Nucleotide sequence of NDV strain La Sota' CC /note='Nucleotide sequence of NDV strain La Sota' CC /note='Nucleotide sequence of NDV strain La Sota' CC /note='Nucleotide sequence of NDV strain La Sota' CC /note='Nucleotide sequence of NDV strain La Sota' CC Location/Qualifiers FT intron (1)..(121) FT CDS (122)..(1591) FT FT intron (1592)..(1886) FT CDS (1887)..(3074) FT FT intron (3075)..(3289)

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Qy 1921 CGCGCGTTAGCCAAAGTTGCGTTAGAGNATGATGAAGAGAGGCAAAAAATACATGGCGC 1980
Db 6418 CGCGCGTTAGCCAAAGTTGCGTTAGAGNATGATGAAGAGAGGCAAAAAATACATGGCGC 6477
Qy 1981 TTGATATTCCGGATTGCAATCTTATTCTTAACAGTAGTACCTTGGCTTATATCTGTAGCC 2040
Db 6478 TTGATATTCCGGATTGCAATCTTATTCTTAACAGTAGTACCTTGGCTTATATCTGTAGCC 6537
Qy 2041 TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG 2100
Db 6538 TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG 6597
Qy 2101 ATTTCCAGGCGAGAGAAAGATTACATCTACACTTGGTTCCATCAAGATGTAGTAGAT 2160
Db 6598 ATTTCCAGGCGAGAGAAAGATTACATCTACACTTGGTTCCATCAAGATGTAGTAGAT 6657
Qy 2161 AGGATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTAATTAATCTAGACACCA 2220
Db 6658 AGGATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTAATTAATCTAGACACCA 6717
Qy 2221 ATATGAACCAATPAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGG 2280
Db 6718 ATATGAACCAATPAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGG 6777
Qy 2281 TGGGGGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 6778 TGGGGGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 6837
Qy 2341 GATGATCTAGTGATGTCACATCACTTCTATCCCTCTGCTATTTCAAGAACATCTCAATTT 2400
Db 6838 GATGATCTAGTGATGTCACATCACTTCTATCCCTCTGCTATTTCAAGAACATCTCAATTT 6897
Qy 2401 ATCCCGCGCTACTACAGATCAGTTGCTCACTCGAATACCCCTCATTTGACATGAGTCT 2460
Db 6898 ATCCCGCGCTACTACAGATCAGTTGCTCACTCGAATACCCCTCATTTGACATGAGTCT 6957
Qy 2461 ACCATTAAGTCTACACCCATAATGTAATTAATGTTGCTGATGTCAGAGATCACTCAATCA 2520
Db 6958 ACCATTAAGTCTACACCCATAATGTAATTAATGTTGCTGATGTCAGAGATCACTCAATCA 7017
Qy 2521 TATCAGTATTAGCATTGTTGCTCGGACATCTGCAACAGGAGGATTTCTTTCT 2580
Db 7018 TATCAGTATTAGCATTGTTGCTCGGACATCTGCAACAGGAGGATTTCTTTCT 7077
Qy 2581 ACTCGGTTCCATCAACCTGAGACACACCCAAATCGAAGTCTTCAGTGTGAGTGCA 2640
Db 7078 ACTCGGTTCCATCAACCTGAGACACACCCAAATCGAAGTCTTCAGTGTGAGTGCA 7137
Qy 2641 ACTCCCTGGTTGTGATATGCTGTCTCGAAGTCTCGGAGACAGAGAGAAAGATTAT 2700
Db 7138 ACTCCCTGGTTGTGATATGCTGTCTCGAAGTCTCGGAGACAGAGAGAAAGATTAT 7197
Qy 2701 AACTCAGCTGCTTACGCGATGTTACATGGAGGTTAGGTTTCGACGGCCAGTACCAC 2760
Db 7198 AACTCAGCTGCTTACGCGATGTTACATGGAGGTTAGGTTTCGACGGCCAGTACCAC 7257
Qy 2761 GAAAGGACCTAGATGTCAACAACTTATTCGGGACTGGGTTCGCAACTACCCAGGAGTA 2820
Db 7258 GAAAGGACCTAGATGTCAACAACTTATTCGGGACTGGGTTCGCAACTACCCAGGAGTA 7317
Qy 2821 GGGGGTGGATCTTTTATGACCGCGTATGTTCTCAGTCTACGAGGTTTAAACCC 2880
Db 7318 GGGGGTGGATCTTTTATGACCGCGTATGTTCTCAGTCTACGAGGTTTAAACCC 7377
Qy 2881 AATTCAACCACTGACCTGACAGAGAGGAAATATGTGATATACAGCGATACCAATGAC 2940
Db 7378 AATTCAACCACTGACCTGACAGAGAGGAAATATGTGATATACAGCGATACCAATGAC 7437
Qy 2941 ACATGCCAGATGACCAAGACTACAGATTGCAATGCGCAAGTCTTCGTATAGCCCTGGA 3000
Db 7438 ACATGCCAGATGACCAAGACTACAGATTGCAATGCGCAAGTCTTCGTATAGCCCTGGA 7497
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Qy 3001 CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAGGTGTCAACATCCTTA 3060
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Qy 3061 GGGAAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 3120
Db 7558 GGGAAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 7617
Qy 3121 AGAATTTCAAGTAGGAGATCTCATTTCTTGTATCAACGAGGGTCAATATCTTCT 3180
Db 7618 AGAATTTCAAGTAGGAGATCTCATTTCTTGTATCAACGAGGGTCAATATCTTCT 7677
Qy 3181 CCAGCGTTATATATCTTATGACAGTCAAGCAAAACAGCCACTCTTCATAGTCCCTAT 3240
Db 7678 CCAGCGTTATATATCTTATGACAGTCAAGCAAAACAGCCACTCTTCATAGTCCCTAT 7737
Qy 3241 ACATTCAATGCTTCACTCGGCCAGGATGATATCCCTTGCAGGCTTCAGCAAGATGCCCC 3300
Db 7738 ACATTCAATGCTTCACTCGGCCAGGATGATATCCCTTGCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTATCTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTATCTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 7855

RESULT 2
AR492934 15186 bp DNA linear PAT 15-MAY-2004
LOCUS Sequence 134 from patent US 6719979.
DEFINITION AR492934
ACCESSION AR492934
VERSION AR492934.1 GI:47264085
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15186)
AUTHORS Peeters,B.P.H., de Leeuw,O.S. and Gielkens,A.L.J.
TITLE Newcastle disease virus infectious clones, vaccines and diagnostic assays
JOURNAL Patent: US 6719979-A 134 13-APR-2004;
FEATURES Location/Qualifiers
source 1..15186
/mol_type="genomic DNA"

ORIGIN
Query Match 99.9%; Score 3353.2; DB 6; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTAGAAGATTCTGGATCCCGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Db 4498 ACGGGTAGAAGATTCTGGATCCCGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557
Qy 61 TTCTACCAAGAACCCAGCACCTATGATCTGCTATCCGGGTTCCGCTGGCAGTCTGAGTTG 120
Db 4558 TTCTACCAAGAACCCAGCACCTATGATCTGCTATCCGGGTTCCGCTGGTACTGAGTTG 4617
Qy 121 CATCTGTCGGGCAAACTCCATTTGATGGCAGGCTCTTTGACAGTGCAGGAATTGTGGTTAC 180
Db 4618 CATCTGTCGGGCAAACTCCATTTGATGGCAGGCTCTTTGACAGTGCAGGAATTGTGGTTAC 4677
Qy 181 AGGAGACAAACCGCTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240
Db 4678 AGGAGACAAACCGCTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT 4737
Qy 241 CTTCCCGAATCTGCCAAGGATTAAGGAGGATGTGCGAAAGCCCTTGGATGCATACAA 300
Db 4738 CTTCCCGAATCTGCCAAGGATTAAGGAGGATGTGCGAAAGCCCTTGGATGCATACAA 4797
Qy 301 CAGGACATTCACCACTTGTCTACCCCTTGTGACTCTATCCGTAGGATACAAAGATC 360
Db 4798 CAGGACATTCACCACTTGTCTACCCCTTGTGACTCTATCCGTAGGATACAAAGATC 4857
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QY	361	TGTGACTACATCTGGAGGGGGAGACAGAGGGCGCCTTATAGGCGCCATTATTGCGGGTGT	420
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QY	421	GGCTCTTGGGGTTCGAACCTGCCGCAAAATAACAGCGCGCGAGCTCTGATACAAAGCCAA	480
Db	4918	GGCTCTTGGGGTTCGAACCTGCCGCAAAATAACAGCGCGCGAGCTCTGATACAAAGCCAA	4977
QY	481	ACAAAATGCTGCCAAACATCTCCGACTTAAAGAGAGACATTGCCGCAACCAATGAGGCTGT	540
Db	4978	ACAAAATGCTGCCAAACATCTCCGACTTAAAGAGAGACATTGCCGCAACCAATGAGGCTGT	5037
QY	541	GCAATGAGGTCACCTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT	600
Db	5038	GCAATGAGGTCACCTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT	5097
QY	601	TGTTAATGACCAATTTAATAAAACAGCTCAGGAAATAGACTGCATGATCAAAATTTGCAACGCA	660
Db	5098	TGTTAATGACCAATTTAATAAAACAGCTCAGGAAATAGACTGCATGATCAAAATTTGCAACGCA	5157
QY	661	AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTTCGGACCAAAAT	720
Db	5158	AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTTCGGACCAAAAT	5217
QY	721	CACCTTCACCTGCTTTAAAACAAAGCTGACTATTTCAGGCACCTTTTCAAACTTAGCTGGTGAAA	780
Db	5218	CACCTTCACCTGCTTTAAAACAAAGCTGACTATTTCAGGCACCTTTTCAAACTTAGCTGGTGAAA	5277
QY	781	TATGGAATTAATTGACTAAGTTAGGTGAGGAAACAATCAACTCAGCTCATTAATTCGG	840
Db	5278	TATGGAATTAATTGACTAAGTTAGGTGAGGAAACAATCAACTCAGCTCATTAATTCGG	5337
QY	841	TAGCGCTTAATCACCGGTAAACCTTCTATACGACTCACAGACTCAACTCTTGGGTAT	900
Db	5338	TAGCGCTTAATCACCGGTAAACCTTCTATACGACTCACAGACTCAACTCTTGGGTAT	5397
QY	901	ACAGGTAACCTTCACTTCAGTCGGGAACCTTAAATAATATGCGTGGCCACCTTACTTGGAAAC	960
Db	5398	ACAGGTAACCTTCACTTCAGTCGGGAACCTTAAATAATATGCGTGGCCACCTTACTTGGAAAC	5457
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QY	1021	GGTCGGTCTGTGATAGAGAACTTGACACCTCATCTGATAGAACTGACTTAGATT	1080
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QY	1081	ATATTGTACAAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	1140
Db	5578	ATATTGTACAAGAAATAGTAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	5637
QY	1141	CAATAAGTCGGCTGTATGTACTCAAAAGACCGAAGCGCACTTACTACACCATATGAC	1200
Db	5638	CAATAAGTCGGCTGTATGTACTCAAAAGACCGAAGCGCACTTACTACACCATATGAC	5697
QY	1201	TATCAAGGTTCACTCATCGCCAACTTCAGAGATGACCAATGTAGATGTGTAAACCCCCC	1260
Db	5698	TATCAAGGTTCACTCATCGCCAACTTCAGAGATGACCAATGTAGATGTGTAAACCCCCC	5757
QY	1261	GGGTATCATATCGCAAACTTATGGAGAACCGGTGTCTCTAATAGATAAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAACTTATGGAGAACCGGTGTCTCTAATAGATAAAACAATCATGCAA	5817
QY	1321	TGTTTATTCCTTAGGGGGATATCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
Db	5818	TGTTTATTCCTTAGGGGGATATCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	5877
QY	1381	GAAGATATCTCAATCAAGATTTCTCAAGTAAATAAACAAGGCAATCTTGATATCTCAAC	1440
Db	5878	GAAGATATCTCAATCAAGATTTCTCAAGTAAATAAACAAGGCAATCTTGATATCTCAAC	5937

QY	1441	TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATACTTAGAGGAAGCA	1500
Db	5938	TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATACTTAGAGGAAGCA	5997
QY	1501	CAGAAACTAGACAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATAT	1560
Db	5998	CAGAAACTAGACAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATAT	6057
QY	1561	CGTTTTGACTATCATATCTCTTGTGTTTGGTATATCTTAGCCTGATTCTAGCATGCTACCT	1620
Db	6058	CGTTTTGACTATCATATCTCTTGTGTTTGGTATATCTTAGCCTGATTCTAGCATGCTACCT	6117
QY	1621	AATGTACAAAGCAAAAGCGCAACAAAAACCTTTATTTATGGCTTTGGAAATAATCTCTAGA	1680
Db	6118	AATGTACAAAGCAAAAGCGCAACAAAAACCTTTATTTATGGCTTTGGAAATAATCTCTAGA	6177
QY	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	6237
QY	1741	TAATTTGTGTGAAAAGTTCTGTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAAAATCTACGGT	1800
Db	6238	TAATTTGTGTGAAAAGTTCTGTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAAAATCTACGGT	6297
QY	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACCGGTAAAGAGAGCGCGCCCTCAATTC	1860
Db	6298	TGTAGATGACCAAGGACGATATACGGGTAGAACCGGTAAAGAGAGCGCGCCCTCAATTC	6357
QY	1861	GAGCCAGGCTTACAAACCTTCGTTCTACCGCTTACCGCAACAGCTCCTCAATCATGGAC	1920
Db	6358	GAGCCAGGCTTACAAACCTTCGTTCTACCGCTTACCGCAACAGCTCCTCAATCATGGAC	6417
QY	1921	CGCGCGTTAGCCAAAGTTCGGTTAGAGAATGATGAAGAGAGGCAAAAAATACATGCGCG	1980
Db	6418	CGCGCGTTAGCCAAAGTTCGGTTAGAGAATGATGAAGAGAGGCAAAAAATACATGCGCG	6477
QY	1981	TTGATATTCGGATTCGAATCTTATTTTAAACAGTGTGACCTTGCTGTATCTGTAGCC	2040
Db	6478	TTGATATTCGGATTCGAATCTTATTTTAAACAGTGTGACCTTGCTGTATCTGTAGCC	6537
QY	2041	TGCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG	2100
Db	6538	TGCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG	6597
QY	2101	ATTTCCAGGCGCAGAGAAAGATTACATCTACATCTTGGTTCCAAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGCGCAGAGAAAGATTACATCTACATCTTGGTTCCAAATCAAGATGTAGTAGAT	6657
QY	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTTGAGACACA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTTGAGACACA	6717
QY	2221	ATTTGAAACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGGG	2280
Db	6718	ATTTGAAACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGGG	6777
QY	2281	TGGGGGCGCACCTTATCCATGACCCAGATTTATATAGGGGGGATAGGCAAGAACTCATTTGTA	2340
Db	6778	TGGGGGCGCACCTTATCCATGACCCAGATTTATATAGGGGGGATAGGCAAGAACTCATTTGTA	6837
QY	2341	GATGATGTAGTGTGATGTCATCATTTCTATCCCTCTGCAATTTCAAGAAATCTGGAATTTT	2400
Db	6838	GATGATGTAGTGTGATGTCATCATTTCTATCCCTCTGCAATTTCAAGAAATCTGGAATTTT	6897
QY	2401	ATCCCGGCGCCTTACTACAGGATCAGGTTGCACTCGAATACCTCTCATTTTACATGAGTGT	2460
Db	6898	ATCCCGGCGCCTTACTACAGGATCAGGTTGCACTCGAATACCTCTCATTTTACATGAGTGT	6957
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Db	6958	ACCCATTACTGTCTACACCCCATTAATTAATTTGTCTGGATGCAAGATCACTCACATTTCA	7017
QY	2521	TATCAGTATTTAGCACTTGGTGTGCTCCGGACATCTGCAACAGGGAGGGTATTTCTTTCT	2580

Db	7018	TATCAGTATTAGACATTGGTGTCTCGGACATCTGCAACAGGAGGTATCTTTCT	7077
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Db	7078	ACTCTGGCTTCCATCAACTCGACACACCCAAAATCGGAAGTCTTCGAGTGTGAGTGCA	7137
Qy	2641	ACTCCCTCGGTTGTGATATGCTGTCTGCGAAGTACGAGAGACAGAGGAAGAAGATTAT	2700
Db	7138	ACTCCCTCGGTTGTGATATGCTGTCTGCGAAGTACGAGAGACAGAGGAAGAAGATTAT	7197
Qy	2701	AACTCAGCTGCCCTACGCGATGATACATCGGAGGTTAGGTTTCGACGGCCAGTACCAC	2760
Db	7198	AACTCAGCTGCCCTACGCGATGATACATCGGAGGTTAGGTTTCGACGGCCAGTACCAC	7257
Qy	2761	GAAGAAGACCTAGATGTCAACAACATTATTCGGGGACCTGGGTGGCAACTACCCAGGAGTA	2820
Db	7258	GAAGAAGACCTAGATGTCAACAACATTATTCGGGGACCTGGGTGGCAACTACCCAGGAGTA	7317
Qy	2821	GGGGTGGATCTTTTATTGACAGCCGGCTATGGTTCTCAGTCTACGAGGTTAAAAACC	2880
Db	7318	GGGGTGGATCTTTTATTGACAGCCGGCTATGGTTCTCAGTCTACGAGGTTAAAAACC	7377
Qy	2881	AATTCAACCCAGTACACTGTACAGGAAGGAAATATGTATATACAGCGATACAATGAC	2940
Db	7378	AATTCAACCCAGTACACTGTACAGGAAGGAAATATGTATATACAGCGATACAATGAC	7437
Qy	2941	ACATGCCAGATGAGCAAGACTACAGATTGCAATGCGCAAGTCTTCGTATAAGCCCTGGA	3000
Db	7438	ACATGCCAGATGAGCAAGACTACAGATTGCAATGCGCAAGTCTTCGTATAAGCCCTGGA	7497
Qy	3001	CGGTTTGGTGGAAACCGATACAGACAGCTATCTTATCTATCAAGGTGTCAACATCCTTA	3060
Db	7498	CGGTTTGGTGGAAACCGATACAGACAGCTATCTTATCTATCAAGGTGTCAACATCCTTA	7557
Qy	3061	GGCGAAGACCGGTACTGACTGTACCGCCCAACACAGCTCACACTCATGGGGCCGAAGGC	3120
Db	7558	GGCGAAGACCGGTACTGACTGTACCGCCCAACACAGCTCACACTCATGGGGCCGAAGGC	7617
Qy	3121	AGAAATCTCAGTAGGGACATCTCATTTCTGTATCAACAGGGGTCAATCATCTTCTCT	3180
Db	7618	AGAAATCTCAGTAGGGACATCTCATTTCTGTATCAACAGGGGTCAATCATCTTCTCT	7677
Qy	3181	CCCGGTTATTATCTTATGACAGTACAGCAACAAAACAGCACTCTTCTATAGTCTTAT	3240
Db	7678	CCCGGTTATTATCTTATGACAGTACAGCAACAAAACAGCACTCTTCTATAGTCTTAT	7737
Qy	3241	ACATTCAATGCTTCACTCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC	3300
Db	7738	ACATTCAATGCTTCACTCGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC	7797
Qy	3301	AACCTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358
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RESULT 3	
AX008510	
LOCUS	AX008510 15186 bp DNA linear PAT 06-SEP-2000
DEFINITION	Sequence 162 from Patent WO9966045.
ACCESSION	AX008510
VERSION	AX008510.1 GI:9996061
KEYWORDS	
SOURCE	Newcastle disease virus
ORGANISM	Newcastle disease virus
REFERENCE	1
AUTHORS	Gielkens, A.L., Koch, G., De Leeuw, O. and Peeters, B.P.
TITLE	Newcastle disease virus infectious clones, vaccines and diagnostic assays
JOURNAL	Patent: WO 9966045-A 162 23-DEC-1999; GIELKENS ARNOUD LEONARD JOSEF (NL); KOCH GUUS (NL); LEEUW OLAV SVEN

DE (NL); PEETERS BERNARDUS PETRUS HUBER (NL); STICHTING DIENST LANDBOUWKUNDI (NL)	FEATURES
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intron	6206. .6411																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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Db	5638	CAATACGTGGCCCTGTATGTTACTCAAGACCGAAGGCGCACTTACTACCATACATGAC	5697
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Db	6298	TGTATAGTGAACAAAGGACGATATACGGGTGAAGCGGTAAAGAGAGCGCCGCCCTCAATGC	6357
Qy	1861	GAGCCAGGCTTCAACACTCGTTCTACCGCTTCAACGCAACAGTCTCAATCATGAC	1920
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Qy	1921	CGCCCGTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAAAATACATGGCG	1980
Db	6418	CGCCCGTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAAAATACATGGCG	6477
Qy	1981	TTGATATTCGGATGCAATCTTATCTTAAACAGTAGTACCTTGGCTTATCTGTAGCC	2040
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Qy	2041	TCCCTTTTATATAGATGGGGCTAGCACACCTAGCCATCTTGTAGGCATACCGACTAGG	2100
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Db	6598	ATTTCCAGGCGAGAAGAAAAGATTACATCTACCTTGGTTCCATCAAGATGTAGTAGAT	6657
Qy	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTTGAGACCACA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTTGAGACCACA	6717
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Db	6718	ATTATGAACCGAATAACATCTCTCTTATCAGATTTAATGGAGCTGCAACAAACAGTGGG	6777
Qy	2281	TGGGGGGCACTATCCATGACCCAGATTTATATAGGGGGGATAGCAAAAGAACTCATTTGTA	2340
Db	6778	TGGGGGGCACTATCCATGACCCAGATTTATATAGGGGGGATAGCAAAAGAACTCATTTGTA	6837
Qy	2341	GATGATGCTAGTATGATGTCACATCATCTTATCCCTCTGCAATTTCAAGAAACATCTGAAATTT	2400
Db	6838	GATGATGCTAGTATGATGTCACATCATCTTATCCCTCTGCAATTTCAAGAAACATCTGAAATTT	6897
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Qy	2461	ACCCATTTATGCTACACCCCAATATATGTTGCTGGATGCGAGATCACTCAATTCACATTC	2520
Db	6958	ACCCATTTATGCTACACCCCAATATATGTTGCTGGATGCGAGATCACTCAATTCACATTC	7017
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Qy	3061	GGCGAAGACCCGTTACTGACTGTACCGCCCAACACAGTCACTCATGCGGCGCGAAGGC	3120
Db	7558	GGCGAAGACCCGTTACTGACTGTACCGCCCAACACAGTCACTCATGCGGCGCGAAGGC	7617
Qy	3121	AGAAATCTCAGTGTAGGGACATCTCATTCTTGTATCAACGAGGGTCACTCATCTCTCT	3180
Db	7618	AGAAATCTCAGTGTAGGGACATCTCATTCTTGTATCAACGAGGGTCACTCATCTCTCT	7677
Qy	3181	CCCGCGTTATTTATCTCCTATGACAGTCAAGCAAAACAGCCACTCTTCATAGTCTTAT	3240
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Qy	3241	ACATTCATGCTTACTCGGCGAGGTAGTATCCCTTGGCAGGCTTCAGCAAGATGCCCC	3300
Db	7738	ACATTCATGCTTACTCGGCGAGGTAGTATCCCTTGGCAGGCTTCAGCAAGATGCCCC	7797
Qy	3301	AACCTCGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358
Db	7798	AACCTCGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	7855

VPSTNFKRKEKKIQHNTRYGBELFTRLCTHIEKKLGLSSWNNVPRSEPSIRTD PAFWHSKSTAKPAMHLTKQIORHLWMAAKTSAANKLVMLTHKGVQVFPVLPVLVV THNENKFTCLTLOELVYADMMKEDWNIISTTAVHLRSSEKIDDLTDLALAK DLGNQVYDVVLEMEGFAYGAVOLLEPSGTFAGFANFQELQELDIILGLLPNDIAESV THAIAVTFSGLEONQAEMLCILRLHGLPLESRIAAKVRQMCAPKMDVPMIQLQV LSPFKGTIINGYRKNAGVWPKVDIYGVKVGOLHADSABISHDMLREYKLSAL EPEPCIEYDPVIMWFLKDKAIAHPNDNWLASFRNLISEDOKKHVKATSTNRLLI EFLESNDFOPTKMESELYLTLEYLRDNDNAVVSYSLEKEVKVNGRIFAKUTKLURNQV MAEGILADQIAPFQNGVQIDSISLTKSMLAMSQLSFNSNKKRIITDKERVSSNRNH DPKSKRRRVATEITTDLOKYCLNWRQYIKLFAHAINOLMGLPHFFEWIIHLRMDIT MFVGDPNPSDDPDCDLSPVNDIYIVSARGGIEGLQCKLWMLISIAAIOLAARS HCRVACMVQGDNOVIATVRSRSDSPVMTOLHOASDFEKLHVNHLIGHLNKD REIRSDITFYKRIKFOGAILISQVLKNSKLVLSGDLSENVMSCANIASTVARL CENGLPKOPIYRIMSCVQTFYDFSEFSTNNSHPLDNQSMWIEDISFVHSYVLTFAQ LGSLNLQYSLRYLNRIDPGTFAFAIEKLEAVGLLSPNIMNITLIPRNGMDWASL ENDPYGFNETVASPNVLKHKHTQVLFETCSNPILSGVHTEDNEAEKALAFELNQ ENVHPVAHAIMEASVGRKQIQGLVDTNTVIKIALRTPLIGIKRLMRIVNYSMH AMLPDRDVSRSRSHPLVSNMCSLTADYABNRWSPLTGGRKILGVSNPDITELV EGEILSVSGCTKCDSDGEQFTWFLPSPNIELTDDTSKPPPMRVYLGSKTQERRAAS LAKIAHMSHVKAALRASSVLIWAYGDNEVNWTAALTIAKSRCNVNLEYLRLLSPLPT AGNLOHRLDDGITQMTFTPASLYRCHLTFTYPMILKGCSLKESKRGMMFTNRMLLG LSLIESITPMTTTRTDEITLHLHNSFSCCIREAPVAVPELILGVVPELRTVTSNKF YDPSVSEGDFAELDAIAPKSYELNLESPTIELMNLISISGKLIGOSVUSVDEBTS IKNDALIVDNTNRNISEAQNSDVRLFEYAALEVLLDCSYQLYILRVGLDNILVLM GDIYKMPGILLNIAATISHPVIRSLRHAVGNHDSHQDLADTDFIEMSAKLIVSC TRRIVISGLYSGNKYIDLFPFSLVDNLRNKLQILSLCLLYTLVLFATREIPKIRGT AEEKSCLTLEYLLSDRAVKPLSPDVSSIMSPNIITFPANLYTMSRKSMLIRERDR DITLALLFPDELPPELVODIGARVKDPPTROPAAFOELDSLAPRYDAFTLSQIH PELTSNPEDPILVRLYFPGITGTASSWYKASHLSVPEVRCARHGNSILABSGAI MSLELHVPHETIYNTLFSNEMPNQRHPPTQFOLNSVYVRNLOAETCKDGVQ EFLPMWRENTESDLDKAVGYITSAVPYRSVSLDKHDEIIPGNSQSLDQALNL SLIAMSREGGVYIIKVLAMGYIFHLLMNFAPCSTGYILNSYACRGDMECYLV FVNGYLGDPFHEVVRMAKTLOVRHGTLLSKDEITLRLFTSQORVTDILSSPL RLIKRKNIDTLEAGGQVPRFOAESLVSTLANITQITQIASHDITVRSVLYM EARGDLADTVLETPVNLSTDGKKRSLIOCTQILLEVITLGLRVNLANKIGDIISLV LKGMISWEDLIPRTYVLRKHSTCPKYLKAVLIGITKLEMFTDTSVLVITRAQQFMYKT IGNAVKGYISNCDUS"	Db	4918	GGCTCTTGGGTTGCAACTGCCGCAAAATAACAGCGCGCAGCTCTTGATACAAGCCAA	4977
481	ACAAAATGTCGCAACATCCTCGCATTAAGAGAGACATTTGCCGCAACCAATGAGCTGT	Qy	540	
4978	ACAAAATGTCGCAACATCCTCGCATTAAGAGAGACATTTGCCGCAACCAATGAGCTGT	Db	5037	
541	GCATGAGGTCACTGACGGATTAATCGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT	Qy	600	
5038	GCATGAGGTCACTGACGGATTAATCGCAACTAGCAGTGGCAGTTGGGAAGATGACAGATT	Db	5097	
601	TGTTAATGACCAATTTAATAAAAAACAGCTCAGGAATTAGACTGCATCAAAAATTGCACAGCA	Qy	660	
5098	TGTTAATGACCAATTTAATAAAAAACAGCTCAGGAATTAGACTGCATCAAAAATTGCACAGCA	Db	5157	
661	AGTTGCTAGAGCTCAACTGTAACCGAATTTGACTACAGTATTCGACACACAAT	Qy	720	
5158	AGTTGCTAGAGCTCAACTGTAACCGAATTTGACTACAGTATTCGACACACAAT	Db	5217	
721	CACCTCACCTGCTTTAAAACAGCTGACTATTACGGCACCTTACAATCTAGCTCGTGAAA	Qy	780	
5218	CACCTCACCTGCTTTAAAACAGCTGACTATTACGGCACCTTACAATCTAGCTCGTGAAA	Db	5277	
781	TATGGAATTACTTATGACTAAGTTAGGTGTAGGGAACAAATCAACTCAGCTCATTAATCGG	Qy	840	
5278	TATGGAATTACTTATGACTAAGTTAGGTGTAGGGAACAAATCAACTCAGCTCATTAATCGG	Db	5337	
841	TAGCGCTTAAATCACCGGTAACCTTATCTATACGACTACAGACTCAACTCTTGGGTAT	Qy	900	
5338	TAGCGCTTAAATCACCGGTAACCTTATCTATACGACTACAGACTCAACTCTTGGGTAT	Db	5397	
901	ACAGGTAACTCTACCTTCAGTCGGGAACCTTAATAATATATCGTCCGACCTTCTGGAAC	Qy	960	
5398	ACAGGTAACTCTACCTTCAGTCGGGAACCTTAATAATATATCGTCCGACCTTCTGGAAC	Db	5457	
961	CTTATCCGTAAGCAACCAACAGGGGATTTGCCTCGCACCTTGTCCCAAAAGTGTGACACA	Qy	1020	
5458	CTTATCCGTAAGCAACCAACAGGGGATTTGCCTCGCACCTTGTCCCAAAAGTGTGACACA	Db	5517	
1021	GGTCGGTCTGTGATAGAGAACTTGACACCTCATATCTGTATAGAACTGACTAGATT	Qy	1080	
5518	GGTCGGTCTGTGATAGAGAACTTGACACCTCATATCTGTATAGAACTGACTAGATT	Db	5577	
1081	ATATTGTACAGAAATAGTAACGTTCCCTATGTCCTCGGTGATTTATTCCTGCTTGACGG	Qy	1140	
5578	ATATTGTACAGAAATAGTAACGTTCCCTATGTCCTCGGTGATTTATTCCTGCTTGACGG	Db	5637	
1141	CAATACGTCGGCTGTATGTACTCAAAAGACCGAAGCGCACTTACTACACATACATGAC	Qy	1200	
5638	CAATACGTCGGCTGTATGTACTCAAAAGACCGAAGCGCACTTACTACACATACATGAC	Db	5697	
1201	TATCAAAGGTTCACTCATCGCCAACTGCAAGATGCAACAATGTAGATGTGTAAACCCCC	Qy	1260	
5698	TATCAAAGGTTCACTCATCGCCAACTGCAAGATGCAACAATGTAGATGTGTAAACCCCC	Db	5757	
1261	GGGTATCATATCGCAAAACTATGAGAGAGCGGTGTCTCTAATAGATATAAATCATGCAA	Qy	1320	
5758	GGGTATCATATCGCAAAACTATGAGAGAGCGGTGTCTCTAATAGATATAAATCATGCAA	Db	5817	
1321	TGTTTTATCCTTAGCGGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	Qy	1380	
5818	TGTTTTATCCTTAGCGGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	Db	5877	
1381	GAAGAATATCTCAATCAAGATTCTCAAGTAAATAAACAAGGCAATCTTGATATCTCAAC	Qy	1440	
5878	GAAGAATATCTCAATCAAGATTCTCAAGTAAATAAACAAGGCAATCTTGATATCTCAAC	Db	5937	
1441	TGAGCTTGGGAATGTCAAACATTCGATCAGTATGCTTTTGAATAAGTTAGAGGAAGCAA	Qy	1500	
5938	TGAGCTTGGGAATGTCAAACATTCGATCAGTATGCTTTTGAATAAGTTAGAGGAAGCAA	Db	5997	
1501	CAGAAACTAGACAAAGTCAATGTCAAACCTGACTAGCACATCTGCTCTCTATTACTATAT	Qy	1560	
5998	CAGAAACTAGACAAAGTCAATGTCAAACCTGACTAGCACATCTGCTCTCTATTACTATAT	Db	6057	

ORIGIN

Query Match	99.98;	Score	3353.2;	DB	14;	Length	15186;
Best Local Similarity	99.98;	Pred. No.	0;				
Matches	3355;	Conservative	0;	Mismatches	3;	Indels	0;
Gaps	0;						
Qy	1	ACGGGTAGAAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGAC	60				
Db	4498	ACGGGTAGAAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGAC	4557				
Qy	61	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGCGCTGAGTTG	120				
Db	4558	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGCGCTGAGTTG	4617				
Qy	121	CATCTGTCGGCAAACTCCATTGATGCGAGCGCTCTTTCGAGCTGCGAGAAATGTGGTTAC	180				
Db	4618	CATCTGTCGGCAAACTCCATTGATGCGAGCGCTCTTTCGAGCTGCGAGAAATGTGGTTAC	4677				
Qy	181	AGGAGACAAAGCCGTCACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240				
Db	4678	AGGAGACAAAGCCGTCACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	4737				
Qy	241	CTTCCCGAATCTGCCAAGGATAGAGGAGATGTGCGAAAGCCCCCTTGGATGCATACAA	300				
Db	4738	CTTCCCGAATCTGCCAAGGATAGAGGAGATGTGCGAAAGCCCCCTTGGATGCATACAA	4797				
Qy	301	CAGGACATTCACCACTTTGCTACCCCTTGGTGACTCTATCCGTAGGATACAAAGATC	360				
Db	4798	CAGGACATTCACCACTTTGCTACCCCTTGGTGACTCTATCCGTAGGATACAAAGATC	4857				
Qy	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGGCTTTATAGCGCCCATTTATGCGGGTGT	420				
Db	4858	TGTGACTACATCTGGAGGGGGAGACAGGGCGGCTTTATAGCGCCCATTTATGCGGGTGT	4917				
Qy	421	GGCTCTTGGGTTGCAACTGCGCGCAAAATAACAGCGCGCGAGCTCTGTATACAAGCCAA	480				

QY	1561	CGTTTGGACTATCATATCTCTTGTGTTTGGTATACCTTAGCCTGATTCCTAGCATGCTACCT	1620
Db	6058	CGTTTGGACTATCATATCTCTTGTGTTTGGTATACCTTAGCCTGATTCCTAGCATGCTACCT	6117
QY	1621	AATGTACAAGCAAAAGCGCAACAAAAACCTTATATGCTTGGGAATTAATATCTCPAGA	1680
Db	6118	AATGTACAAGCAAAAGCGCAACAAAAACCTTATATGCTTGGGAATTAATATCTCPAGA	6177
QY	1681	TCAGATGAGACCACTACAAAATGTGAACACAGATGAGAAACGAAAGGTTTCCCTTAATAG	1740
Db	6178	TCAGATGAGACCACTACAAAATGTGAACACAGATGAGAAACGAAAGGTTTCCCTTAATAG	6237
QY	1741	TAATTTTGTGCAAAAGTTCTCGTAGTCTGTGTCAGTTTCAAGAGAGTTAAAGAAAAAATACCGGT	1800
Db	6238	TAATTTTGTGCAAAAGTTCTCGTAGTCTGTGTCAGTTTCAAGAGAGTTAAAGAAAAAATACCGGT	6297
QY	1801	TGTAGATGACAAAGGACGATATACCGGTTAGAAATGATGAAGAGAGCGCCCTCAATTCG	1860
Db	6298	TGTAGATGACAAAGGACGATATACCGGTTAGAAATGATGAAGAGAGCGCCCTCAATTCG	6357
QY	1861	GAGCCAGGCTTCAACCTCGGTTCTACCGCTTACCGCAACAGTCCTCAATCATGGAC	1920
Db	6358	GAGCCAGGCTTCAACCTCGGTTCTACCGCTTACCGCAACAGTCCTCAATCATGGAC	6417
QY	1921	CGCGCGGTTAGCCAAAGTTGCGTTAGAAATGATGAAGAGAGCAAAAAATACATGGCG	1980
Db	6418	CGCGCGGTTAGCCAAAGTTGCGTTAGAAATGATGAAGAGAGCAAAAAATACATGGCG	6477
QY	1981	TTGATATTCGGATTCGAATCTTATTTTAAACAGTAGTACCTTGGCTATATCTGTAGCC	2040
Db	6478	TTGATATTCGGATTCGAATCTTATTTTAAACAGTAGTACCTTGGCTATATCTGTAGCC	6537
QY	2041	TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGCATGG	2100
Db	6538	TCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGCATGG	6597
QY	2101	ATTTCCAGGCGAGAGAAAGATTACATCTACACTTGTGTTCCCAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGCGAGAGAAAGATTACATCTACACTTGTGTTCCCAATCAAGATGTAGTAGAT	6657
QY	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCAATGTTAAATACTGAGACACA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCAATGTTAAATACTGAGACACA	6717
QY	2221	ATTATGACCGCATATACATCTCTCTTATCAGATTAAATGGAGCTGCAACACAGTGGG	2280
Db	6718	ATTATGACCGCATATACATCTCTCTTATCAGATTAAATGGAGCTGCAACACAGTGGG	6777
QY	2281	TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTGTA	2340
Db	6778	TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTGTA	6837
QY	2341	GATGATGCTAGTAGTGCATCATCTATPCCCTCTGCAATTCGCAAGCAATCTGAATTT	2400
Db	6838	GATGATGCTAGTAGTGCATCATCTATPCCCTCTGCAATTCGCAAGCAATCTGAATTT	6897
QY	2401	ATCCCGCGCTACTACAGATCAGGTGCACTGCAATACCCCTCATTTGACATGAGTCT	2460
Db	6898	ATCCCGCGCTACTACAGATCAGGTGCACTGCAATACCCCTCATTTGACATGAGTCT	6957
QY	2461	ACCCATTACTGCTACACCCATAATGTAATTCCTGGATGACAGATCACTCACATTCA	2520
Db	6958	ACCCATTACTGCTACACCCATAATGTAATTCCTGGATGACAGATCACTCACATTCA	7017
QY	2521	TATCAGTATTAGCATTTGGTGTGCTCCGGACATCTGCAACAGGAGGGTATCTTTTCT	2580
Db	7018	TATCAGTATTAGCATTTGGTGTGCTCCGGACATCTGCAACAGGAGGGTATCTTTTCT	7077
QY	2581	ACTCTGGTTCATCAACCTGGACGACACCCAAAAATCGGAAGTCTTGCAGTGTGAGTGCA	2640
Db	7078	ACTCTGGTTCATCAACCTGGACGACACCCAAAAATCGGAAGTCTTGCAGTGTGAGTGCA	7137

QY	2641	ACTCCCTCGGTTGTGATGTCTGCTCGAAAGTCACGAGACACAGAGGAAGAAGATTAT	2700
Db	7138	ACTCCCTCGGTTGTGATGTCTGCTCGAAAGTCACGAGACACAGAGGAAGAAGATTAT	7197
QY	2701	AATCTAGCTGTCCCTACGCGGATGGTACATGGGAGGTTAGGGTTCGACGGCCAGTACCAC	2760
Db	7198	AATCTAGCTGTCCCTACGCGGATGGTACATGGGAGGTTAGGGTTCGACGGCCAGTACCAC	7257
QY	2761	GAAAAGGACCTAGATGCTCAACATTATTTCGGGGAAGTGGTGGCCAACTACCCAGAGTA	2820
Db	7258	GAAAAGGACCTAGATGCTCAACATTATTTCGGGGAAGTGGTGGCCAACTACCCAGAGTA	7317
QY	2821	GGGGGTGGATCTTTTATTGACAGCCGCTATGGTTCTCAGTCTTACGGAGGGTTAAAAACC	2880
Db	7318	GGGGGTGGATCTTTTATTGACAGCCGCTATGGTTCTCAGTCTTACGGAGGGTTAAAAACC	7377
QY	2881	AATTCAACAGTGACACTGTGTACAGGAAGGAATAATGTGTATATACAAGCGATACAATGAC	2940
Db	7378	AATTCAACAGTGACACTGTGTACAGGAAGGAATAATGTGTATATACAAGCGATACAATGAC	7437
QY	2941	ACATGCCAGATGAGCAAGACTACCAAGATTTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA	3000
Db	7438	ACATGCCAGATGAGCAAGACTACCAAGATTTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA	7497
QY	3001	CGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGCAACATCCTTA	3060
Db	7498	CGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGCAACATCCTTA	7557
QY	3061	GGCGAAGACCCGGTACTGTAACGCGCAACACAGTCACTATGCGGGCCGGAAGGC	3120
Db	7558	GGCGAAGACCCGGTACTGTAACGCGCAACACAGTCACTATGCGGGCCGGAAGGC	7617
QY	3121	AGAAATTCACAGTAGGAGCATCTCAATTTCTTGTATCAAGGGGTCACTACTTTCTCT	3180
Db	7618	AGAAATTCACAGTAGGAGCATCTCAATTTCTTGTATCAAGGGGTCACTACTTTCTCT	7677
QY	3181	CCCGCTTATATATCTCTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCCTTAT	3240
Db	7678	CCCGCTTATATATCTCTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCCTTAT	7737
QY	3241	ACATTCAATGCTTCACTCGGCAAGTATGCCCTTGGCAAGCTTCAGCAAGATCCCC	3300
Db	7738	ACATTCAATGCTTCACTCGGCAAGTATGCCCTTGGCAAGCTTCAGCAAGATCCCC	7797
QY	3301	AACCTGCTGTACTGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC	3358
Db	7798	AACCTGCTGTACTGAGTCTATACAGATCCATATCCCTAATCTTCTATAGAAACC	7855

NDV18898 15186 bp RNA linear VRL 20-DEC-1999
Newcastle disease virus cDNA to complete genomic RNA, clone 30.
Y18898
Y18898.1 GI:5578883
F gene; fusion protein; hemagglutinin-neuraminidase; HN gene; L gene; large protein; M gene; matrix protein; NP gene; nucleocapsid protein; P gene; phosphoprotein.
Newcastle disease virus
Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.

1
Romer-Oberdorfer, A., Mundt, E., Mebatsion, T., Buchholz, U. J. and Mettenleiter, T. C.
Generation of recombinant lentogenic Newcastle disease virus from cDNA
J. Gen. Virol. 80 (Pt 11), 2987-2995 (1999)
20047980
10580061
2 (bases 1 to 15186)
Romer-Oberdorfer, A.
Direct Submission

RESULT 5
NDV18898
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE

CENGLPKDFCYLYNIMSCVQTYFDSEFSITNNSHFDLQSWIEDISFVHSYVLTPAQ
LGLSLNLOYRSLYTRNIGDPGTAFABEIKRLEAVGLLSPNIMTNILTRPGNDWASL
CNDPYSNPFETVASPINLVLKHTTORVLFCETSNPLISGVHTEDENEAEKALAEFLANQ
EVHPVVAHAIMBASVGRERKQJQLVDVTNTVIKIALTRPLGIGIKRLMRIVNYSWH
AMLFDDVDFSSNSRPLVSSNNCSLTLADYARNRWSPLTGGKRLKLGVSNPDTIELV
EGSILSVSGCTRLCDGDEQFTWFLHPSNIELTDDTSKNPPMRPVLYGSKLQERRAAS
LAKIAHMSPHVKAALRASSVLWAYGDNEVNWTAALTIAKSRCNVNLVRLRLLSPLEPT
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YDSPVSEGDPAFLDLATFKSYELNLESYPTIELMNLISISSGKLQGSVVSDEDTYS
IKNDALIVDNTNRSEASONSDVRLFEYALLEVLLDCSYQJLYLRGLDNLNVLMS
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TRRVIISGLYSGNKYDLIFPSVDLNNLNEKMLQISRLCCLYTLFVATREIPKIRGLT
AEBKCSLTLBYLLSDAVKPLLSPOVSSIMSPNIITFPANLYMYSKSLNLIREDRDR
DTLIALLPPELLEPSVODIGARVKDPEPTROPAAFLQELDLASAPRYDAFTLSOIH
PELTSNPEDYLRVILFRGIGTASSWKASHLLSVPEVRCARHNSLYLAGSGSAI
MSLLEUHPHETIYNTLFSNEMNPPRHFPTPTQLNSVYVYNNIOAEVTCKDGQVQ
EPRPLRENTESDLSDKVGYITSAPYRSVSLHLHDEIEIPGNSQLLDQJLAINL
SLJAMHSVEGGVVIKVLVAMGYFPHLLMNLFPAPGSTRGYILNSGYACRGMCEYLIV
FVMGYLGGPTFVHEVVRMAKTLVORHGTLLSKSDEITLRLFTFSQORVTDILSSPLP
RLJKYLKKNIDTALIEAGOPVRPFCAESILVSTLANITOLITIIASHIDTVIRSVLYM
EASGDLDADTVLFTFPYNLSTDGKRTSLKQCTROIILEVILGLRVENLNKIGDIIISIV
LKMISMEDLIPRLTLKHSTCPKYLKAVLIGITKULKEMFTDTSVLYLTRAQOKPYMKT
IGNAVRGYSNCDNS"

ORIGIN

Query Match		99.98;	Score 3353.2;	DB 14;	Length 15186;			
Best Local Similarity		99.98;	Pred. No. 0;					
Matches 3355;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;			
Qy	1	ACGGGTAGAAAGATTCTG	GATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60				
Db	4498	ACGGGTAGAGATTCTGG	ATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557				
Qy	61	TTCTACCAAGAACCCAG	CACCTATGATGCTGACTATCCGGGTTGCGCTGGCAGTCAAGTTG	120				
Db	4558	TTCTACCAAGAACCCAG	CACCTATGATGCTGACTATCCGGGTTGCGCTGGTACTGAGTTG	4617				
Qy	121	CATCTGTCCGGCAAACT	CCATTCGATGCGAGCCCTCTTGACAGCTGCAGGAATTCGGTTAC	180				
Db	4618	CATCTGTCCGGCAAACT	CCATTCGATGCGAGCCCTCTTGACAGCTGCAGGAATTCGGTTAC	4677				
Qy	181	AGGAGACAAAGCCGCT	CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240				
Db	4678	AGGAGACAAAGCCGCT	CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	4737				
Qy	241	CCTCCCGAAATCTGCC	CAAGGATAGGAGGAGCATGTGCGAAAGCCCCCTTGGATGCATACAA	300				
Db	4738	CCTCCCGAAATCTGCC	CAAGGATAGGAGGAGCATGTGCGAAAGCCCCCTTGGATGCATACAA	4797				
Qy	301	CAGGACATTGACCACAT	TTTGCTCACCCCCCTTTGGTGACTCTATCCGTAGGATACAAGAGTC	360				
Db	4798	CAGGACATTGACCACAT	TTTGCTCACCCCCCTTTGGTGACTCTATCCGTAGGATACAAGAGTC	4857				
Qy	361	TGTGACTACATCTGGAG	GGGGGAGACAGGGGCGCCTTATAGGGCCCAATTTATGGCGGTGT	420				
Db	4858	TGTGACTACATCTGGAG	GGGGGAGACAGGGGCGCCTTATAGGGCCCAATTTATGGCGGTGT	4917				
Qy	421	GGCTCTTTGGGGTTGCA	ACTGCGCGCAAAATAACAGCGGCGCAGCTCTGTATACAAGCCAA	480				
Db	4918	GGCTCTTTGGGGTTGCA	ACTGCGCGCAAAATAACAGCGGCGCAGCTCTGTATACAAGCCAA	4977				
Qy	481	ACAAAATGCTGCCAAAT	CTCTCCGACTTAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	540				
Db	4978	ACAAAATGCTGCCAAAT	CTCTCCGACTTAAGAGAGCATTTGCCGCAACCAATGAGGCTGT	5037				
Qy	541	GCATGAGGTCACTGACCG	GAATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTT	600				
Db	5038	GCATGAGGTCACTGACCG	GAATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTT	5097				
Qy	601	TGTTAATGACCAATTTT	AATAAAACAGCTCAGGAATTAGACTGCATCAAAAATTCACAGCA	660				
Db	5098	TGTTAATGACCAATTTT	AATAAAACAGCTCAGGAATTAGACTGCATCAAAAATTCACAGCA	5157				

Qy	661	AGTTGGGTAGAGCTCAAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCACAAAAT	720
Db	5158	AGTTGGGTAGAGCTCAAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCACAAAAT	5217
Qy	721	CACCTTCACTGCTTTTAAAACAAGCTGACTATTACAGGCACCTTTTACAATCTAGCTGGTGAAA	780
Db	5218	CACCTTCACTGCTTTTAAAACAAGCTGACTATTACAGGCACCTTTTACAATCTAGCTGGTGAAA	5277
Qy	781	TATGGATTACTTATTGACCTAAAGTTAGGTAGGGACAATCACTCAGCTCATTAATCGG	840
Db	5278	TATGGATTACTTATTGACCTAAAGTTAGGTAGGGACAATCACTCAGCTCATTAATCGG	5337
Qy	841	TAGCGCTTAATCAACCGGTAAACCTATTCTATACGACTCACAGACTCAACTCTTTGGGTAT	900
Db	5338	TAGCGCTTAATCAACCGGTAAACCTATTCTATACGACTCACAGACTCAACTCTTTGGGTAT	5397
Qy	901	ACAGGTAACCTCTACCTTCAGTCGGGAACCTAAATAATATGCGGTGCCACCTACTTTGGAAC	960
Db	5398	ACAGGTAACCTCTACCTTCAGTCGGGAACCTAAATAATATGCGGTGCCACCTACTTTGGAAC	5457
Qy	961	CTTATCCGTAAGCACAAACGAGGGATTTCGCTCGGCACCTTGTCCCAAAAAGTGGTGACACA	1020
Db	5458	CTTATCCGTAAGCACAAACGAGGGATTTCGCTCGGCACCTTGTCCCAAAAAGTGGTGACACA	5517
Qy	1021	GGTCGGTTCCTGTGATAGAAAGAACTTCACACCTCATACTGTATAGAAACTGACTTAGATTT	1080
Db	5518	GGTCGGTTCCTGTGATAGAAAGAACTTCACACCTCATACTGTATAGAAACTGACTTAGATTT	5577
Qy	1081	ATATTGTAACAAGAAATAGTAAACGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAGCGG	1140
Db	5578	ATATTGTAACAAGAAATAGTAAACGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAGCGG	5637
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VERSION	AY225110.1	GI:28824865	
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SOURCE	Newcastle disease virus		
REFERENCE	Viruses: ssRNA negative-strand viruses; Mononegavirales;		
AUTHORS	Paramyxoviridae; Paramyxovirinae; Avulavirus.		
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	Pan, Z.S., Chen, Y.D., Shao, H.B., Yang, J., Xiong, Z.L., Wen, G.Y. and		
	Zhang, C.Y.		
TITLE	Complete sequence for HB92 strain of Newcastle disease virus		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 15186)		
AUTHORS	Pan, Z.S., Chen, Y.D., Wen, G.Y. and Zhang, C.Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JAN-2003) Institute of Virology, Department of Life		
	Science, Wuhan University, Wuhan, Hubei 430072, China		
REFERENCE	3 (bases 1 to 15186)		
AUTHORS	Shao, H.B., Yang, J. and Xiong, Z.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JAN-2003) Institute of Animal Husbandry and		
	Veterinary Science, Hubei Academy of Agricultural Science, Wuhan,		
	Hubei 430209, China		
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RESULT 7

AF375823 LOCUS AF375823 15186 bp RNA linear VRL 06-NOV-2001
DEFINITION Newcastle disease virus strain B1 isolate Takaaki, complete genome.
ACCESSION AF375823

VERSION	AF375823.1	GI:14190062
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SOURCE	Newcastle disease virus B1	
ORGANISM	Viruses; sRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.	
REFERENCE	1 (bases 1 to 15186)	
AUTHORS	Nakaya,T., Cros,J., Park,M.S., Nakaya,Y., Zheng,H., Sagrera,A., Villar,E., Garcia-Sastre,A. and Palese,P.	
TITLE	Recombinant Newcastle disease virus as a vaccine vector	
JOURNAL	J. Virol. 75 (23), 11868-11873 (2001)	
MEDLINE	21548317	
PUBMED	11689668	
REFERENCE	2 (bases 1 to 15186)	
AUTHORS	Nakaya,T., Garcia-Sastre,A. and Palese,P.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-MAY-2001) Microbiology, Mount Sinai School of Medicine, One Gustave Levy Place, New York, NY 10029, USA	
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ORIGIN

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DEFINITION	Newcastle disease virus B1, complete genome.		
ACCESSION	AF309418		
VERSION	AF309418.1	GI:11527326	
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SOURCE	Newcastle disease virus B1		
ORGANISM	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.		
REFERENCE	1 (bases 1 to 15186)		
AUTHORS	Sellers,H.S. and Seal,B.S.		
TITLE	Complete sequence for the B1 strain of Newcastle disease virus		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 15186)		
AUTHORS	Sellers,H.S. and Seal,B.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-SEP-2000) U.S. Department of Agriculture/Agriculture Research Services, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA		
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ORIGIN

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RESULT 9
AY289002
LOCUS
DEFINITION
ACCESSION

3819 bp mRNA linear
AY289002 Newcastle disease virus turkey/USA/VGGA/89 fusion protein and hemagglutinin-neuraminidase bicistronic mRNA, complete cds.
AY289002

VERSION	AY289002.1	GI:33772483	
KEYWORDS	Newcastle disease virus		
SOURCE	Newcastle disease virus		
ORGANISM	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.		
REFERENCE	1 (bases 1 to 3819)		
AUTHORS	Seal,B.S.		
TITLE	Nucleotide and predicted amino acid sequence analysis of the fusion protein and hemagglutinin-neuraminidase protein genes among Newcastle disease virus isolates. Phylogenetic relationships among the Paramyxovirinae based on attachment glycoprotein sequences		
JOURNAL	Funct. Integr. Genomics 4 (4), 246-257 (2004)		
PUBMED	15108051		
REFERENCE	2 (bases 1 to 3819)		
AUTHORS	Seal,B.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-MAY-2003) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA		
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Best Local	Similarity 98.6%;	Pred. No. 0;	
Matches 3310;	Conservative 0;	Mismatches 48;	Indels 0; Gaps 0;
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QY	121	CATCTGTCCGGCAAACTCCATTTGATGGCAGGCTCTTTGCAGCTGCAGGAATTTGGTTAC	180
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RESULT 10

A03663

LOCUS

DEFINITION Newcastle disease virus HN and F genes.

A03663 3825 bp DNA linear

PAT 13-DEC-1993

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2101 ATTTCCAGGCGAAGAAAAGATTACATCTACACTTGGTTTCCAAATCAAGATGTAGTAGAT 2160
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2221 ATTATGAACCAATAACATCTCTCTTATCAGATTAATGAGCTGCGAACCAACAGCGGG 2280
2281 TGGGGGCGACCTATCCATGACCCAGATTTATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
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2461 ACCAATTTACTGCTACACCTCAATTAATGTAATTTGCTGATGTCAGAGATCACTCAATCA 2520
2521 TATCAGTATTTAGCAGCTTGGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTCT 2580
2521 TATCAGTATTTAGCAGCTTGGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTCT 2580
2581 ACTTGGGTTCCATCAACCTTGGACGACACCCAAATCGGAAGTTTTCAGGTGTGAGTGA 2640
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2641 ACTCCCTGGGTTGTGATATGCTGTCTGAAAGTTCAGGAGACAGAGGAAGAATTTAT 2700
2641 ACTCCCTGGGTTGTGATATGCTGTCTGAAAGTTCAGGAGACAGAGGAAGAATTTAT 2700
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3181 CCGCGTTTATATATCTATGACAGTCAAGCAACAAACAGGCTCTTCTAGTCTTAT 3240
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3301 AACTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358

RESULT 11
E01252
LOCUS
DEFINITION Synthetic DNA encoding Newcastle disease virus (NDV) protein.
ACCESSION E01252

E01252 3825 bp DNA linear PAT 29-SEP-1997
LOCUS
DEFINITION Synthetic DNA encoding Newcastle disease virus (NDV) protein.
ACCESSION E01252

VERSION	E01252.1	GI:2169511	
KEYWORDS	JP 1987163693-A/1.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 3825)		
AUTHORS	Richiyaado,U.B., Fuiritsupu,C., Piitaa,T.E. and Neiru,S.M.		
TITLE	NEWCASTLE DISEASE VIRUS GENE CLONE		
JOURNAL	Patent: JP 1987163693-A 1 20-JUL-1987;		
COMMENT	NATL RES DEV CORP		
	OS Artificial gene		
	OC Newcastle disease virus (NDV)		
	PN JP 1987163693-A/1		
	PD 20-JUL-1987		
	PF 18-DEC-1986 JP 1986302719		
	PR 18-DEC-1985 GB 85 8531147, 14-APR-1986 GB 86 8609037, PR		
	15-JUL-1986 US 86 885765		
	PI RICHIVAADO UOOKAA BINGAMU, FUIRITSUPU CHIYANBAZU, PI PIITAA		
	TANREI EMAASON.		
	PI NEIRU SUTUYUWAATO MIRAA		
	PC C12N15/00,C12N1/20/A61K39/17,C12P21/02,(C12N1/20,C12R1.19);		
	CC strandedness: Double;		
	CC topology: Linear;		
	CC hypothetical: No;		
	CC anti-sense: No;		
	CC *source: strain=Bodet-C;		
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	FH 3'UTR 1..47		
	FT join(48..1708),(1915..3648)		
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	FT protein'		
	FT 5'UTR 3649..3825		
	FT mRNA 1..3825		
	FT exon 1..1708		
	FT intron 1709..1914		
	FT exon 1915..3825.		
FEATURES	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
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Best Local Similarity	97.0%;	Pred. No. 0;	
Matches 3257;	Conservative	0; Mismatches 101;	Indels 0; Gaps 0;
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Db	1	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCTAGGTGCAAGATGGGCCCCAGACC	60
QY	61	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG	120
Db	61	TTCTACCAAGAACCCAGTACTATGATGCTGACTGTCCGAGTCGCGCTGCTAGTTG	120
QY	121	CATCTGTCCGGAAACTCCATTGATGCGAGGCGCTTTGCGAGCTGCGAGGAATTTGGTTAC	180
Db	121	CATCTGTCCGGAAACTCCATTGATGCGAGGCGCTTTGGCGGCTGCGAGGAATTTGGTTAC	180
QY	181	AGGAGACAAAGCGTGAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Db	181	AGGAGACAAAGCGTGAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
QY	241	CCTCCGGAATCTCCCAAGGATAAGGAGGATGTCGGAAGCCCCCTTGGATCATACAA	300
Db	241	CCTCCCAAACTCCCAAGGATAAGGAGGATGTCGGAAGCCCCCTTGGATCATACAA	300
QY	301	CAGGACATTGACCACTTTGCTACCCCTTTGGTGAATCTATCCGTAGGATACAAAGTTC	360
Db	301	CAGGACATTGACCACTTTGCTACCCCTTTGGTGAATCTATCCGTAGGATACAAAGTTC	360

361	QY	TGTGACTACATCTGGAGGGGGAGACAGGGGGCCCTTATAGCGCCATTATTATGGCGGTGT	420
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421	Db	GGCTCTGGGGTTGCAACTGCTGCAAAATAACAGGGCGCGAGCTCTGATACAGGCCAA	480
481	QY	ACAAATGCTGCGCAACATCCTCGACTTAAAGAGAGCATTTAGGCTGCATCAGAAATTGCA	540
481	Db	ACAAATGCTGCGCAACATCCTCGACTTAAAGAGAGCATTTAGGCTGCATCAGAAATTGCA	540
541	QY	GCATGAGGTCACTGACCGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGT	600
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601	Db	TGTTAATGACCAATTTAATAAACAAGCTCAGGAATTAGGCTGCATCAGAAATTGCAAGCA	660
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661	Db	AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCCAAAT	720
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721	Db	CACCTCACCTGCTTTAAACAAGCTGACTATTAGGCACTTTTACAATCTAGCTGGTGGAA	780
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781	Db	TATGATTAATTAATGACTAAGTTAGTTAGGTAGGGAACAATCAACTCAGCTCATTAATCGG	840
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841	Db	TAGCGGCTTAATCAACCGGTAACCCCTATTCTGACGACTCAGAGCTCAACTCTTGGGTAT	900
901	QY	ACAGGTAACTCTACCTTTCAGTCGGGAACCTAAATAATATATCGTGGCCACCTACTTGGAAAC	960
901	Db	ACAGGTAACTCTACCTTTCAGTCGGGAACCTAAATAATATATCGTGGCCACCTACTTGGAAAC	960
961	QY	CTTATCCGTTAAGCAACACAGGGGATTTGCTCGGCACTTTGTGCCAAAAGTGGTGCACAC	1020
961	Db	CTTATCTGTAAGCAACACAGGGGATTTGCTCGGCACTTTGTGCCAAAAGTGGTGCACAC	1020
1021	QY	GGTCGGTCTGTGATAGAGAACTTGACACCTCATATCTATAGAGAACTGACTTACATTT	1080
1021	Db	GGTCGGTCTGTGATAGAGAACTTGACACCTCATATCTATAGAGAACTGACTTACATTT	1080
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1081	Db	ATATTGTACAAGAAATAGTAACATTCCTATGTCCTGGTATTTATTCCTGCTTGAACGG	1140
1141	QY	CAATACGTGGGCTGTATGTAATCAAGACCGAAGCGCACTTATACACCATATATGAC	1200
1141	Db	CAATACATCGGCTGTATGTAATCAAGACCGAAGCGCACTTATACACCATATATGAC	1200
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1201	Db	TATCAAGGTTTCAAGTATCGCAACCTGCAAGATGCAACATGTAGATGTAAACCCCCC	1260
1261	QY	GGGTATCATATCGCAAACTATGGAGAGCCGCTGCTCTAAATAGATAAACAATCATGCAA	1320
1261	Db	GGGTATCATATCGCAAACTATGGAGAGCCGCTGCTCTAAATAGATAAACAATCATGCAA	1320
1321	QY	TGTTTATCTTATAGCGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTAATCTATCA	1380
1321	Db	TGTTTATCTTATAGCGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTAATCTATCA	1380
1381	QY	GAAGATATCTCAATACAGATTCTCAAGTAAATAACAGGCAATCTTGTATCTCAAC	1440
1381	Db	GAAGATATCTCAATACAGATTCTCAAGTAAATAACAGGCAATCTTGTATCTCAAC	1440
1441	QY	TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTTGAATAAGTTAGAGGAAAGCAA	1500

Db 1441 |||||TGAGCTTGGGATGTCACAACTCGATCAGTAATGCTTTGANTAGTTAGAGGAACAA 1500
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Qy 1801 TGTAGATGACCAAGGACGATATACGGGTAGAACGGTAAAGAGGCGCGCCCTCAATTGC 1860
Db 1801 TGTAGATGACCAAGGACGATATACGGGTAGAACGGTAAAGAGGCGCGCCCTCAATTGC 1860
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Db 1861 GAGCAGGCTTCAACACCTCGGTTCTACCGCTTACCGCAACAGAGTCTCAATCATGGAC 1920
Qy 1921 CGCGCGTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGCAAAAAATACATGGCGC 1980
Db 1921 CGCGCAGTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGCAAAAAATACATGGCGC 1980
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Db 2521 CATCAGTATTTAGCATTGGTGTGCTCCGGACAACCTGCAACAGGAGGATATTTCTTTCT 2580
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Db 2821 GGGGTTGGATCTTTTATTGACAGCCGGTATGTTCTCAGTCTACGAGGGGCTGAAAACCC 2880
Qy 2881 AATTACCCAGTGCACACTGTACAGGAAGGAAATATGTGATATACAAGCGATACAATGAC 2940
Db 2881 AATTACCCAGTGCACACTGTACAGGAAGGAAATATGTGATATACAAGCGATACAATGAC 2940
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Db 3001 CGGTTTGGTGGGAAAACGATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCCTTG 3060
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Db 3301 AACTCGTGTGTTACTGGAGTCTATACAGATCCCATATCCCTTAATCTTCTATAGAAACC 3358

RESULT 12

AY289000

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AY289000 4552 bp mRNA linear VRL 04-OCT-2004
Newcastle disease virus chicken/USA/Roakin/48 fusion protein and
hemagglutinin-neuraminidase bicistronic mRNA, complete cds.
AY289000
AY289000.1 GI:33772477
Newcastle disease virus
Newcastle disease virus
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Avulavirus.
Seal, B.S.
Nucleotide and predicted amino acid sequence analysis of the fusion
protein and hemagglutinin-neuraminidase protein genes among
Newcastle disease virus isolates. Phylogenetic relationships among
the Paramyxovirinae based on attachment glycoprotein sequences

JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	Funct. Integr. Genomics 4 (4), 246-257 (2004) 15108051 2 (bases 1 to 4552) Seal, B-S Direct Submission Submitted (01-MAY-2003) Agricultural Research Service, USDA, Southeast Poultry Research Laboratory, 934 College Station Road, Athens, GA 30605, USA	Db	301	CAGGACATTGACACACTTTGCTCACCCCCCTTGGTGACTCTATCCGCTAGGATACAAGAGTC	360
FEATURES	Location/Qualifiers	Qy	361	TGTGACTACATCTGAGGGGGGAGACAGAGGGGCGCTTATAGGCGCCATTTATTTGGCGGTGT	420
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		Qy	481	ACAAATGCTGCCAATCTCCGACTTAAAGAGAGCATTTGGCGAACCAATGAGGCTGT	540
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		Db	661	AGTTGGTGTAGAGTCAACCTGTACTACCGAATTTGACTACAGTATTCGGACCCACAAAT	720
		Qy	721	CACCTCACCTGCTTTAAACAAGCTACTATTAGGCACTTTTCAATCTAGCTGGTGGAAA	780
		Db	721	CACCTCACCTGCTTTAAACAAGCTACTATTAGGCACTTTTCAATCTAGCTGGTGGAAA	780
		Qy	781	TATGATTAATTTGACTAAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTT	840
		Db	781	TATGATTAATTTGACTAAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTT	840
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		Qy	901	ACAGGTAACTTACCTTTCAGTGGGAACTTAATAATATGCGGTGGCCACCTACTTGGAAAC	960
		Db	901	ACAGGTAACTTACCTTTCAGTGGGAACTTAATAATATGCGGTGGCCACCTACTTGGAAAC	960
		Qy	961	CTTATCCGTAAGCAACACAGGGGATTTCCCTCGGCACTTTGCTCCCAAAAAGTGGTGACAC	1020
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		Qy	1021	GGTGGTCTGTGTATGAGAACTTGCACCTCATCTCTATAGAACTGCAGCTTAGATTT	1080
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		Qy	1081	ATATTGTAAGAAATAGTAACGTTCCCTATGTCCTGGTATTATTCTCTGCTTGGCGG	1140
		Db	1081	ATATTGTAAGAAATAGTAACATTCCTATGTCCTGGTATTATTCTCTGCTTGGCGG	1140
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		Db	1141	CAATACGTCGGCTGTATGTACTCAAGACCCGAAAGCGCACTTACTACCAATACATGAC	1200
		Qy	1201	TATCAAGGTTTCACTGCACATCGCAAGATGACAAATGTAGATGTGTAAACCCCCC	1260
		Db	1201	TATCAAGGTTTCACTGCACATCGCAAGATGACAAATGTAGATGTGTAAACCCCCC	1260
		Qy	1261	GGGTATCATATCGCAAACTATGGAGAGCGGTCTCTAAATAGATAAAACAATCATGCAA	1320
		Db	1261	GGGTATCATATCGCAAACTATGGAGAGCGGTCTCTAAATAGATAAAACAATCATGCAA	1320
		Qy	1321	TGTTTTATCTTTAGCGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTATCTTATCA	1380
		Db	1321	TGTTTTATCTTTAGCGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTATCTTATCA	1380
		Qy	1381	GAAGAAATCTCAATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
		Db	1381	GAAGAAATCTCAATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440

ORIGIN

Query Match	95.0%;	Score 3190;	DB 14;	Length 4552;
Best Local Similarity	96.9%;	Pred. No. 0;		
Matches 3253;	Conservative 0;	Mismatches 105;	Indels 0;	Gaps 0;
QY	1	ACGGGTAGAGATTC	TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	1	ACGGGTAGAGATTC	TGGATCCCGGTTGGCGCTTCTTAGGTGCAAGATGGGCCCCAGACC	60
QY	61	TTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG	120	
Db	61	TTCTACCAAGAACCCAACCTATGATGCTGACTGTCGGGTGCGCTGGTACTGAGTTG	120	
QY	121	CATCTGTCGGGCAAACTCCATTGATGGCAGGCTCTTGGCAGCTGCGAGGAATTTGGTTAC	180	
Db	121	CATCTGTCGGGCAAACTCCATTGATGGCAGGCTCTTGGCGCTGCGAGGAATTTGGTTAC	180	
QY	181	AGGAGACAAAGCGCTCAACATATACAGCTCATCCAGACAGGATCAATCATAGTTAAGCT	240	
Db	181	AGGAGACAAAGCAGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240	
QY	241	CCTCCCGAATCTGCCCAAGGATAAGGAGGATGTGCGAAAGCCCCCTTGGATGCATACAA	300	
Db	241	CCTCCCAACCTGCCCAAGGATAAGGAGGATGTGCGAAGAGCCCCCTTGGATGCATACAA	300	
QY	301	CAGGACATTGACCACTTGTCTACCCCCCTTGGTGACTCTATCCGTAGGATACAAGAGTC	360	

Qy	1441	TGAGCTTGGGAATGTCAAACACTCGATCAGTAAGTCTTTGAATGAAGTTT	GAGGAAAGCAA	1500
Db	1441	TGAGCTTGGGAATGTCAAACACTCGATCAGTAAGTCTTTGAATGAAGTTT	GAGGAAAGCAA	1500
Qy	1501	CAGAAACTAGACAAAGTCAATGTCAAACTAGCAGTACACATCTGCTCTCAATACCTATAT	1560	
Db	1501	CAGAAACTAGACAAAGTCAATGTCAAACTAGCAGTACACATCTGCTCTCAATACCTATAT	1560	
Qy	1561	CGTTTTGACATCATATCTCTTGTGTTTTGGTATATCTTAGCTGATTCAGCATGCTACCT	1620	
Db	1561	CGTTTTGACATCATATCTCTTGTGTTTTGGTATATCTTAGCTGATTCAGCATGCTACCT	1620	
Qy	1621	AATGTAACAGCAAAAGCGCAACAAAAAAGCTTTAATATGCTTTGGGAATTAATCTCTAGA	1680	
Db	1621	AATGTAACAGCAAAAGCGCAACAAAAAAGCTTTAATATGCTTTGGGAATTAATACCTCTAGA	1680	
Qy	1681	TCAGATGAGGCGCACTACAAAAATGTGAAACACAGATGAGGACGAAAGGTTTCCTTAATAG	1740	
Db	1681	TCAGATGAGGCGCACTACAAAAATGTGAAACACAGATGAGGACGAAAGGTTTCCTTAATAG	1740	
Qy	1741	TAATTTGTGTGAAAGTTCTGTGTAGTCTGTGAGTTTCAGAGAGTTTAAAGAAAAAATCTACCGGT	1800	
Db	1741	TAATTTGTGTGAAAGTTCTGTGTAGTCTGTGAGTTTCAGAGAGTTTAAAGAAAAAATCTACCGGT	1800	
Qy	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACGGTAAAGAGAGCGCGCCCTCAATTCG	1860	
Db	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACGGTCCGAGAGCGCGCCCTCAATTCG	1860	
Qy	1861	GAGCCAGGCTTCAAAAGCTCGTTCTACCGTTTCCAGCAGAAAGTCTCAATCTAGGAC	1920	
Db	1861	GAGCCGGGCTTCAAAAGCTCGTTTACCGCTTCCAGCAGAGCAGTCTCTCAGTCAATGGAC	1920	
Qy	1921	CGCGCGCTTAGCCAAAGTTGGTTAGAGAAATCATGAAAGAGGCGCAAAAAATACATGCGCG	1980	
Db	1921	CGCACAGTTAGCCAAAGTTGGTTAGAGAAATCATGAAAGAGGCGCAAAAAATACATGCGCG	1980	
Qy	1981	TTGATATTCGGGATTTGCAATCTTATTTCTTAACAGTAGTGACCTTGGCTATATCTGTAGCC	2040	
Db	1981	TTGATATTCGGGATTTGCAATCTTACTCTTAACAGTAGTGACCTTAGCTACATCTGTAGCC	2040	
Qy	2041	TCCCTTTTATATAGCATGGGGCTTAGCACACCTTAGCCATCTTGTAGGCAATCCGACTAGG	2100	
Db	2041	TCCCTTTTATATAGCATGGGGCTTAGCACACCTTAGCCACCTTGTAGGCAATCCGACCAGG	2100	
Qy	2101	ATTTCCAGGGCAGAAAGATTTACATCTACATCTGTTTCCATCAAGATGTAGTAGAT	2160	
Db	2101	ATTTCCAGGGCAGAAAGATTTACATCTGCACTCTGTTTCCATCAAGATGTAGTAGAT	2160	
Qy	2161	AGGATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATATCTGAGACCA	2220	
Db	2161	AGGATATATAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAACATGAGACTACA	2220	
Qy	2221	ATTTAGAACGCAATTAACATCTCTTTATCAGATTAATGGAGCTGCAAAACACAGTGGG	2280	
Db	2221	ATTTAGAACGCAATTAACATCTCTCTTTATCAGATTAATGGAGCTGCGAACAACAGCGGG	2280	
Qy	2281	TGGGGGCACTATCCATGACCCAGATTTATAGGGGGGATAGGCAAGAACTCATTTGTA	2340	
Db	2281	TGGGGGCACTATCCATGACCCAGATTTATAGGGGGGATAGGCAAGAACTCATTTGTA	2340	
Qy	2341	GATCATCTAGTGATGTCACATCATTTCTATCCCTCTCATTTTCAAGAAACATCTGAAATTTT	2400	
Db	2341	GATCATCTAGTGATGTCACATCATTTCTATCCCTCTCATTTTCAAGAAACATCTGAAATTTT	2400	
Qy	2401	ATCCCGGGCGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATGAGTGCT	2460	
Db	2401	ATCCCGGGCGCTACTACAGGATCAGGTTGCAATCGGATACCTTCATTTGACATGAGTGCT	2460	
Qy	2461	ACCCATTACTGCTACACCCATTAATGTATATTTGCTGGATGCGAGATCACTCACATTTCA	2520	
Db	2461	ACCCATTACTGCTACATCAATATATTAATATCGTCTGGATGCGAGATCACTCACACTCA	2520	

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Db	2521	TATCAGTATTATAGCACTTGGTGTGCTCCGACATCTGCAACAGGAGGGTATTCTTTTCT	2581
Qy	2581	ACTCTGGTTTCCATCAACCTGGACGACACCAAAATCGGAAGTCTTCAGTGTGAGTGCA	2640
Db	2581	ACTCTGGTTTCCATCAACCTGGATGACACCAAGATCAGGAGACAGAGGAAGAATTAT	2640
Qy	2641	ACTCCCCCTGGTTTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGGAAGAATTAT	2700
Db	2641	ACTCCCCCTAGTTTGTGATATGCTGTGCTGAAAGTCAACGAGACAGAGGAAGAATTAT	2700
Qy	2701	AATCAGCTGTCCCTACGCGGATGTATCATGGAGGTTAGGGTTCGAGCGGCAGTACCAC	2760
Db	2701	AATCAGCTGTCCCTACGCTGATGGTATCATGGAGGTTAGGGTTCGAGCGGCATATCCAC	2760
Qy	2761	GAAAGGACCTAGATGTACAAATATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA	2820
Db	2761	GAAAGGACCTAGAGTTCACAAATATTTCGAGACTGGGTGGCCAACTACCCAGGAGTA	2820
Qy	2821	GGGGTGGATCTTTTATTGACGCGCGTATGGTTCTCAGTCTACGGAGGGTTAAAAACC	2880
Db	2821	GGGGTGGATCTTTTATTGACGCGCGTATGGTTCTCAGTCTACGGAGGGTGAACCACC	2880
Qy	2881	AATTACCCAGTGCACCTGTACAGGAAGGAATATGTGATATATCAAGCGATACATGAC	2940
Db	2881	AATTACCCAGTGCACCTGTACAGGAAGGAATATGTGATATATCAAGCGATACAAATGAC	2940
Qy	2941	ACATGCCAGATGAGCAAGACTACCCAGATTTCGATGGCCAAAGTCTTCGTATAAGCCCGG	3000
Db	2941	ACATGCCAGATGAGCAAGACTACCCAGATCCGAAATGGCCAAAGTCTTCGTATAAGCCCGG	3000
Qy	3001	CGGTTTGGTGGGAAACGCATACAGCGGCTATCTTATCTATCAAGGTGTCAAACATCTCTA	3060
Db	3001	CGGTTTGGTGGGAAACGCATACAGCGGCTATCTTATCTATCAAGGTGTCAAACATCTCTG	3060
Qy	3061	GGCGAAGACCCGGTACTGCTACCGCCCAACACAGTCACTCATGCGGGGCGGAAGGC	3120
Db	3061	GGCGAAGACCCAGTACTGCTACCGCCCAACACAGTCACTCATGCGGGGCGGAAGGC	3120
Qy	3121	AGAAATTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTCTCTCT	3180
Db	3121	AGAAATTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTCTCTCTCT	3180
Qy	3181	CCGCGTTATTATCTATGACAGTCAAGCAACAAACAGCCACTCTTCATAGTCCCTTAT	3240
Db	3181	CCGCGTTATTATCTATGACAGTCAAGCAACAAACAGCCACTCTTCATAGTCCCTTAT	3240
Qy	3241	ACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC	3300
Db	3241	ACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC	3300
Qy	3301	AATCTGTGTGTACTGAGTCTATACAGATCCATATCCCTTATCTCTATAGAAACC	3358
Db	3301	AATCTGTGTGTACTGAGTCTATACAGATCCATATCCCTTATCTCTATAGAAACC	3358
RESULT 13			
NDVFHN		3825 bp	RNA
LOCUS		Newcastle disease virus gene for fusion glycoprotein precursor,	linear VRL 09-JAN-1998
DEFINITION		haemagglutinin-neuraminidase glycoprotein precursor.	
ACCESSION		D00243.1	GI:222174
VERSION			
KEYWORDS		haemagglutinin-neuraminidase glycoprotein precursor; fusion glycoprotein precursor; F; HN; NDV; avirulent.	
SOURCE		Newcastle disease virus	
ORGANISM		Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.	
REFERENCE		1 (bases 1 to 3825)	
AUTHORS		Millar,N.S., Chambers,P. and Emmerson,P.T.	
TITL		Nucleotide sequence of the fusion and haemagglutinin-neuraminidase	

glycoprotein genes of Newcastle disease virus, strain Ulster:
molecular basis for variations in pathogenicity between strains
J. Gen. Virol. 69 (Pt 3), 613-620 (1988)
88171450
3351479
PUBMED

COMMENT
To understand the molecular basis for the differences in virulence
shown by strains of NDV, the sequences of the E and HN genes of the
extremely avirulent strain Ulster were determined and compared with
those of several other NDV strains (discussed in [1]).

FEATURES

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ORIGIN

Query Match 84.2%; Score 2826.8; DB 14; Length 3825;
Best Local Similarity 90.1%; Pred. No. 0;
Matches 3026; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

QY	1	ACGGGTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
DB	1	ACGGGTAGAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGATC	60
QY	61	TTCTACCAAGAACCCAGCATATGATGTGACTATCCGGGTTGCCTGCGCTGAGTTG	120
DB	61	TTCTACCAAGATCCAGTACCTCTGATGCTGACCGTCCGGGTCGCGCTGAGTTG	120
QY	121	CATCTGTCGGGAAATCCCATGATGCGAGCGCTCTTGACGTGCGAGGAATTTGGTTAC	180
DB	121	CGTCTGTCGACAAAGTCCCTTGTATGCGAGCGCTCTTGACGTGCGAGGAATTTGGTTAC	180

Qy	1261	GGGTATCATATCGCAAACTATAGAGAAGCGGTCTCTTAATAGATAAAACAATCATGCAA	1320
Db	1261	GGGTATCATATCGCAAAATATAGAGAAGCTGTGTCTCTAATAGTAGGCAATCATGCAA	1320
Qy	1321	TGTTTTTACCTTAGCGGGATAACTTTAAGGCTCAGTGGGGATTCAGATGTAACCTATATCA	1380
Db	1321	TGTCCTATCCTTAGACGGGAATACTTTGAGGCTCAGTGGGGAAATTTGATGCAACTATATCA	1380
Qy	1381	GAAGAATATCTCAATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
Db	1381	AAAGATATCTCAATACAAGATTCTCAAGTAATCGTGACAGGCAATCTTGATATCTGCAC	1440
Qy	1441	TGAGCTTGGGAATGTCACAACTCGATCAGTAATGCTTTGAAATAAGTTAGAGAAAGCAA	1500
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Qy	1501	CAGAAACTAGACAAAGTCATGTCAAACTGCACCTAGCACATCTGCTCTCATTAACCTATAT	1560
Db	1501	CAGCAAACTAGACAAAGTCAATGTCAAACTGACACAGCACATCCGCTCTCATCAACCTATAT	1560
Qy	1561	CGTTTTGCACTCATATCTCTTGTTTTTGGTATATCTTAGGCTGATTCAGATCTAGCATGCTACCT	1620
Db	1561	CGTTTTAAGTCTATATCTCTTGTTTTTGGTATATCTTAGGCTGATTCAGATGCTACCT	1620
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Db	1621	GATGTAACAAGCAAAAGCGCAACAGAAGACCTTGTTATGCTTGGGAATAATAACCTTGA	1680
Qy	1681	TCAGATGAGAGCCACTACAAAAATGTGAAACACAGATGAGGAAACGAGGTTTCCTTAATAG	1740
Db	1681	TCAGATGAGAGCCACTACGAAAAATGTGAAATGTAGATGAGAGGCGGAGGCAATCTCCAATAG	1740
Qy	1741	TAATTTGTGTGAAAGTTCTGTGTAGTCTGTAGTTTCAGAGAGTTTAAGAAAAAACTACCGGT	1800
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Qy	1801	TGTAGATGACCAAAAGGACGATATACGGGTAGAACGGTAAGAGAGGCGCGCCCTCAATTCG	1860
Db	1801	TGTAGATGACCAAAAGGCAACATACGGGTAGAACGGTCAGAGAGGCGCGCCCTCAATCGG	1860
Qy	1861	GAGCCAGGCTTCACAACTCGGTTCTACCGGTTCAACGCAACACAGTCTCTCAATCATGGAC	1920
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Qy	1981	TTGATATTCGGGATTGCAATCTTATCTTAAACAGTAGTAGCTTTGGCTATATCTGTAGCC	2040
Db	1981	TTGGTATTCGGGATCGCGATCCTACTTTTAAACAGTAGTAGCTTTAGCCATCTCTGCGAGCC	2040
Qy	2041	TCCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTTGAGGCAATACCGACTAGG	2100
Db	2041	GCCCTTGCAATATAGTATGGAGGCTAGCACACCTAGCGACCTTATAGGCAATACCGACTGGC	2100
Qy	2101	ATTTCCAGGGCAGAGAAAGAAATACATCTACCTCTGCTTCCAATCAAGATGTAGTAGAT	2160
Db	2101	ATCTTAGACGAGGAAAGAAATACATCTGCACTCTCGGTTCCAAACCAAGATGTAGTAGAT	2160
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Db	2161	AGGATATATAGCAGGTGGCCCTCGAATCTCCATTTGGCATTTGCTTAAACACCGAATCTACA	2220
Qy	2221	ATTTAGAACCGAATAACATCTCTCTCTTATCAGATTAATGAGGCTGCAAAACAACAGTGGG	2280
Db	2221	ATTTAGAACCGAATAAACATCTCTCTTATCAGATCAATGGAGCGCGCAAAATAGCAGCGGG	2280
Qy	2281	TGGGGGCACTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	2340
Db	2281	TGCGGGGCACTATTTCAATGATCCAGATTATATCGGGGGAAATAGGTAAGAAACTTATTTGTA	2340
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[illegible]

RESULT 14
AY562991
LOCUS
DEFINITION

AY562991 15186 bp RNA linear VRL 22-MAR-2004
Newcastle disease virus isolate chicken/N. Ireland/ulster/67,
complete genome.

ACCESSION	AY562991	
VERSION	AY562991.1	GI:45511246
KEYWORDS	Newcastle disease virus	
SOURCE	Newcastle disease virus	
ORGANISM	Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Avulavirus.	
REFERENCE	1 (bases 1 to 15186)	
AUTHORS	Wise, M.G., Kuntz, R.L. and Seal, B.S.	
TITLE	Comparison of full-length genome sequences among the Paramyxoviridae	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 15186)	
AUTHORS	Wise, M.G., Kuntz, R.L. and Seal, B.S.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-MAR-2004) Southeast Poultry Research Laboratory, U.S. Dept. of Agriculture, ARS, 934 College Station Rd., Athens, GA 30605, USA	
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ORIGIN

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VERSION
KEYWORDS
SOURCE
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source

AV741404 15186 bp RNA linear VRL 06-OCT-2004
Newcastle disease virus strain Herts/33, complete genome.
AY741404
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Newcastle disease virus
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Avulavirus.
1 (bases 1 to 15186)
de Leeuw,O.S., Hartog,L., Ravenshorst,N., Koch,G. and
Peeters,B.P.H.
Virulence of Newcastle disease virus is determined by the cleavage
site of the fusion protein and both the stem region and globular
head of the hemagglutinin-neuraminidase protein
Unpublished
2 (bases 1 to 15186)
de Leeuw,O.S. and Peeters,B.P.H.
Direct Submission
Submitted (03-SEP-2004) Infectious Diseases, Wageningen University
and Research Centre, Animal Sciences Group, Edelhertweg 15,
Lelystad, Flevoland 8200 AB, The Netherlands
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IKNDAIIVYDNTNRISEAGNSDVURUFYAALVELLDQSYQLYVLRVGLNNILVLYM
SDLYKNWPGILLNIAATISHPIHSERLNAGLVNHDGSHQADTPIEWSAKLVSC
TRRVVSGLYAGNRYDLLFPVLDNLSSEKMLQILSRLLCCLYVLPATTRIEIKRIGLS
AEEKCSVLTETLSDAVKPLURSEQVSSIMSPNIITPPANLYTMDRSKMLNIREDERD
DTILALFVTEPLDSEFSDQIDGARVKDPTFTRQPAAPVAPVPELIGLAPELRAVTSNKPMS
SEHTLPNPEEDLYRYLFRIGTIGTASSSYKASHLSVPEVRCARHNSLYABESGGA
MSLLEHPHETPIYNTLFGNEMNPPORHFGPTPTPLNSVVRNRYLAQEPYCKGDFQV
EFHPLWRENTSEEDLSKDAVGYITSAVPYRSVSLHCDIEIPGNSQSLDDOLATNL
SLIAHMSVREGGVITKVALYGVYFHLNMLFAPCTKGYILISGNSQACGMDMECYLI
FVMGTGPTFVGVVNRMAKTLVRRHGTLLSKSDEITLRLFTSQOHRVTDLSSPLP
RLMKFLRENTDAILIEAGGQFVPFCAESLVSTLKMOTMTQIASHIDTIVRSVITYM
EAEGDLATVLEFTPNYSLDQKRRTSKQCTRIEVLTLGRKADLNKVGIVGLV
LRGMISLELDILPIRLTIRKSTRCKPYKALVGLITKLEMFDTDTSLLYLTRAQKQPFYMKT
IGNAAKGYNSDNS"

ORIGIN

	Query Match	80.3%	Score 2695.6	DB 14	Length 15186
	Best Local Similarity	87.7%	Pred. No. 0		
	Matches 2944	Conservative 0	Mismatches 414	Indels 0	Gaps 0
Qy	1	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60		
Db	4498	ACGGGTAGAAGAAATTTTGATCCCGTTGGCACATTCAAGGTGCAAGATGGCTCCAGATC	4557		
Qy	61	TTCTACCAAGAAACCCAGCACCTATGATGCTGAATAATCCGGGTTGCGCTGGCAGTGAATTG	120		
Db	4558	TTCTACCAGGATCCCGGTTCCCTCCAATGCTGATCATCCGAATTTGTGTGACGCTGAGTTG	4617		
Qy	121	CATCTGTCCGGCAAACTTCCATTGATGGCAGGCCCTTTGGAGCTGCAGGAATTTGGTTTAC	180		

Db	4618	TATCCGCTCTGACAAAGCTCTCTTGATGGCAGGCGCTCTTGCGAGCTGCGAGGATCGTGTAAAC	4677
QY	181	AGGAGACAAAGCCGCTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Db	4678	AGGAGTAAGCAGTCAACATATACACCTCATCCAGACAGGCTCAATCATAGTCAAGTT	4737
QY	241	CTCCCGAATCTGCCAAGGATGAAGGAGCATGTGCGAAAGCCCCCTTGGATGCATACAA	300
Db	4738	ACTCCCAAAATATGCCAAGGACAAAGAGGCGTGTGCAAAAGCCCCATTTGGAGGCATACAA	4797
QY	301	CAGGACATTCACACATTTGCTACACCCCTTGTGTGACTCTATCCGTTAGATACAGAGTC	360
Db	4798	CAGGACATGCACTACTTTGCTACCCCTTGTGTGATTTCTATCCGAGGATACAGAGTC	4857
QY	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCTTATAGGCGCATTTATTCGCGGTGT	420
Db	4858	TGTGACTACTTCCGGAGGAAGGAGACAGAGCCCTTTATAGGTGCCATTTATCGGCAAGTGT	4917
QY	421	GGCTCTTGGGGTTGCACCTGCGCGCACAAATPACAGGGCGCGCAGCTCTGTATACAAGCCAA	480
Db	4918	AGCTCTTGGGGTTGCACACAGCTGCACAGATAACGGCAGCCCTCGGCCCTGTATACAAGCCAA	4977
QY	481	ACAAATGCTGCCAACATCTCCGACTTAAAGAGAGCATTTGCCGCGCAACCAATGAGGCTGT	540
Db	4978	CCAGAAATGCTGCCAACATCTCCGGCTTAAAGAGAGCATTTGCTGCAACCAATGAAGCTGT	5037
QY	541	GCATGAGTCACTGACGGATTATCGCAACTPAGCAGTGGCAGTTGGGAAGATGCAAGCTT	600
Db	5038	GCAGAGTCACTGACGGATTATCACAACTAGCAGTGGCAGTAGGGAAGATGCAAGCTT	5097
QY	601	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCA	660
Db	5098	TGTTAATGACCAATTTAATAACAGCGCAAGATTTGGACTGTATATAAAATTTACACAGCA	5157
QY	661	AGTTGTTAGAGCTCAACTGTACTTAACCGAATTTGACTACAGTATTCGGACCAAAAT	720
Db	5158	GGTAGGTGTAGAACTCAACTGTGTACCTTAACGTAATTTGACTACAGTATTCGGGCGCAAAAT	5217
QY	721	CACCTCACCTGCTTTAAACAAGCTGACTATTCAGGCACCTTACAATCTAGCTGTGGAA	780
Db	5218	CACCTCCCTGCTTAACTCAGCTGACTATTCAGGCGCTTTACAATTTAGCTGGTGTAA	5277
QY	781	TATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	840
Db	5278	TATGGATTACTTCTGCTGACTAAGTTAGGTGTAGGGAACAACCAACTCAGCTCATTAATCGG	5337
QY	841	TAGCGGCTTAATCACCGGTAAACCTTATCTATAGACTCACAGACTCAACTCTTGGGTAT	900
Db	5338	TAGCGGCTTGATCACCGGCAACCTTATCTGTACGACTCACAGACTCAGATCTTTGGGTAT	5397
QY	901	ACAGGTAACCTCTACCTTCAGTCGGGAACCTTAATAATATATGCGTGCCACCTACTTGGAAAC	960
Db	5398	ACAGGTAACCTTTGCCCTTCAGTCGGGAACCTTAATAATATATGCGTGCCACCTACTTGGAGAC	5457
QY	961	CTTATCCGTAAAGCACCAACAGGGGATTTGCTCGGCACCTTGTCCCAAAAGTGGTGACACA	1020
Db	5458	CTTATCTGTAAAGCACCAACAGGGATTTGCTCAGCAGCTTGTCCCAAAAGTGGTGACACA	5517
QY	1021	GGTCGGTCTGTGATAGAAGAACTTGACACCTCATCTGTATAGAACTGACTTTAGATT	1080
Db	5518	GGTCGGTCTCGTGTATAGAAGAACTTGACACCTCATCTGTATAGGACCGACTTGGATT	5577
QY	1081	ATATTTGACAAAGATAGTACGTTCCCTATGCTCCCTGGTATTATTTCTGCTTGGCGG	1140
Db	5578	ATACTGTACAAAGATAGTACATTTCCCTATGTTCTCTGTTATTATTTCTGCTTGGCGG	5637
QY	1141	CAATAGCTCGGCTGTATGTACTCAAGAACCGAAGCGCACTTACTACACCATACATGAC	1200
Db	5638	TAAATCATCGCTTGCATGTATTTCAAGACTGAAGGCGCACTTACTACGCCATATATGCG	5697
QY	1201	TATCAAAGGTTAGTCACTGCCAACTGCAAGATGACAACTGATGATGTATAACCCGCC	1260
Db	5698	TCTCAAAGGCTCAGTTATTGCCAAATTTGCAAGATGACAACTGTAGATGTGCAAGCCCTCC	5757

QY	1261	GGGTATCATATCGCAAAACTATGGAGAGCCGCTGTCTCTAATAGATAAAACAATCATGCA	1320
Db	5758	GGGTATCATATCGCAAAATTTATGGAGAGCTGTGCTCTTAATAGATAGCACTCATGCAA	5817
QY	1321	TGTTTTATCTTTAGGGGGGATAACTTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
Db	5818	TGTCTTATCTTTAGACGGGATAACTCTGAGGCTCAGTGGGGAATTTGATGCAACCTTATCA	5877
QY	1381	GAAGATATCTCAATAAGATTTCTCAAGTAAATAAAGAGCAATCTTGATATCTCAAC	1440
Db	5878	AAAGATATCTCAATACTAGATTCTCAAGTTATAGTACAGGCAATCTCGATATATCAAC	5937
QY	1441	TGAGCTTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTTGAATAAAGTATAGAGGAAACAA	1500
Db	5938	TGAGCTTTGGGAATGTCAACAACTCAATAAGTAAATGCCCTGATTAAGTATAGGAAAGCAA	5997
QY	1501	CAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCACATCTGTCTCTCAATCACTATAT	1560
Db	5998	CAGAAACTAGACAAAGTCAATGTCAAGCTGACCCAGCACATCTGTCTCTCAATCACTATAT	6057
QY	1561	CGTTTTGACTATCATATCTCTTTGTTTGGTATCTTAGCCTGATTTCTAGCATGCTACCT	1620
Db	6058	CGTTTTAACTGTATATCTCTTTGTTTGGTGTACTTAGCCTGGTTCTAGCATGCTACCT	6117
QY	1621	AATGTACAAAGCAAAAGCGGCAACAAACCACTTATTTATGGCTTGGGAATAAATACTCTAGA	1680
Db	6118	GATGTACAAAGCAAAAGCGGCAACAAACCACTTATTTATGGCTTGGGAATAAATACTCTGA	6177
QY	1681	TCAGATGAGAGCCACTPACAAAATGTGAACAAGATGAGGAACGAAGGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGAGCCACTPACAAAATGTGAACAAGATGAGGAACGAAGGTTTCCCTAATAG	6237
QY	1741	TAATTTGCTGGAAGTTCTGGTAGTCTGTCTCAGTTTCAAGAGTTTAAGAAAATACTACCGGT	1800
Db	6238	CAATTTGCTGGAAGTTCTGCAACACCTGTCAATTTAGAAGAAATTAAGAAAAGCTACTGGA	6297
QY	1801	TGTAGATGACCAAGGACGATATACGGGTAGAAACGGTAAAGAGAGGCGCCCTCAATATGC	1860
Db	6298	TGTAGTGACAAAAGCAATFACAGGTTAGAAACGGTTCGGGAGCCATCCCTCAATCGG	6357
QY	1861	GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTACCGCAACAACAGTCTCAATCATGGAC	1920
Db	6358	GAATCAGGCTCTCATACGCTCTTCTACCGCATCACCAATAGCAAACTTCGGTTATGGAC	6417
QY	1921	CGGCGGTTAGCCAGTTGCGTTAGAGATGATGAAGAGAGGCAAAAATACATCGCGC	1980
Db	6418	CGTGCAAGTTAGCAGAGTTGCGCTAGAGAAATGAAGAAAGAGAGCAAGAAATACATGGCGC	6477
QY	1981	TTGATATTCGGATTGCAATCTTATTTCTTAAACAGTGTAGTACCTTGGCTATATCTGTAGCC	2040
Db	6478	TTTGTATTCGGATCGCAATCTTACTTTTATAGTAAATCACTTAGCCATCTCTGAGCC	6537
QY	2041	TCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTTGTAGGCATACCGACTAG	2100
Db	6538	GCCCTGGTATATAGCATGGAGCTAGCACGCGGGGACCTTGTGGCATACCAACTGTG	6597
QY	2101	ATTTCCAGGGCAGAGAAAAGATTACATCTACACTTGGTTCCCAATCAAGATGTAGTAGT	2160
Db	6598	ATCTCTAGGGCAGAGAAAAGATTACATCTGACCTCAGTTCTTAATCAAGATGTAGTAGAT	6657
QY	2161	AGGATATATAAGCAAGTGGCCCTTGGTCTCGTTGGCATCTGTAAATACTGAGACACA	2220
Db	6658	AGGATATATAGCAGGTGGCCCTTGGTCTCCATTTGGCGTTGCTAAACACTGNATCTGTA	6717
QY	2221	ATTATGAACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAACCAACAGTGGG	2280
Db	6718	ATTATGAATGCAATAACAGTCTCTCTTATCAAAATCAATGGAGCTGCAAAATAATAGCGG	6777
QY	2281	TGGGGGGCACCTTATCCATGACCCAGATTATATAGGGGGATAGGGCAAGAACTCATTTGTA	2340
Db	6778	TGTGGGGCCACTGTTTCATGACCCAGATTACATCGGGGGATAGGGCAAGAACTTATTGTA	6837

2341	Qy	GATGATGCTAGTGAATGTCACATCAATCTATATCCCTCTGCAATTTCAAGAAACATCTGAAATTTT	2400
6838	Db		6897
		GATGACGCTAGTGAATGTCACATCAATCTATATCCCTCTGCGTTCCAAGAAACACCTGAAATTTT	
2401	Qy	ATCCCGCGCGCTACTACAGATCAGGTTGCACTCGAATACCTTCATTTGACATGAGTGCT	2460
6898	Db		6957
		ATCCCGGCACTACTACAGATCAGGTTGCACTCGGATACCTTCATTTGCACTAAGTGCT	
2461	Qy	ACCATTACTGCTACACCCATAATGTAAATATTTGCTGGATGCGAGAGATCACTCACATTTCA	2520
6958	Db		7017
		ACCACCTACTGTTACACTCAATGTGATATATCTGTTGCGAGAGATCACTCACACTCA	
2521	Qy	TATCAGTATTTAGCACTTGGTGCTCCGGACATCTCGAACAGGGAGGTTATCTTTTCT	2580
7018	Db		7077
		CATCAGTACTTAGCACTTGGTGCTTTCCGACATCTCGAACAGGGAGGTTATCTTTTCT	
2581	Qy		2640
		ACTCTGGTTCCATCAACTGGACGACACCCAAATCGGAAGTCTTGCACTGTGAGTGCA	
7078	Db		7137
		ACTCTGGTTCCATCATTTTGGATGACAAACCAAAATCGGAAGTCTTGCACTGTGAGTGCA	
2641	Qy	ACTCCCCTGGTTGTGATATGCTGTGTCGAAAGTCAAGGAGACAGAGGAAGAAGATTAT	2700
7138	Db		7197
		ACTCCCCTAGTGTGTGATATGCTGTCTTAAATACAGAGACTGAGGAAGAAGATTAT	
2701	Qy	AACTCAGCTGTCCTACGCGGATGGTACATGGGAGGTTAGGTTTCGACGCCAGTACCAC	2760
7198	Db		7257
		AGTTTCAGTTACCCCCCATCGATGGTGCAATGAAGGTTAGGTTTGACGGTCAATACCAT	
2761	Qy	GAAGAAGCACTAGATGTCAACAATTATCGGGACCTGGGTGGCCAACTACCCAGGAGTA	2820
7258	Db		7317
		GAGNAGCACTAGACGTCATAACTTTATTTAAGATTGGGTGGCAATTACCCAGGAGTG	
2821	Qy	GGGGTGGATCTTTTATTGACAGCGCGTATGGTTCTCAGTCTACGAGGGTTAAACCC	2880
7318	Db		7377
		GGGGTGGGTCTTTTATTGACACCGCGTGTGGTTCCAGTCTATGAGGGCTTAAACCC	
2881	Qy	AAATTCCACCACTGACACTGTACAGAGAGGGAATATGTGATATACAAGCGATACAATGAC	2940
7378	Db		7437
		AAATTCCGCTAGCAACCGTACAAAGAGGAGATATGTAATATACAAGCGTACAATGAC	
2941	Qy	ACATGCCAGATGAGCAAGACTACAGATTCGAATGGCCAAAGTCTTCGTATAAGCCCTGGA	3000
7438	Db		7497
		ACATGCCAGATGAACAAGATTACCAATTCGATGGCTAAGTCTTCGTATAAGCCCTGGG	
3001	Qy	CGGTTTGGTGGGAACCGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAAATCCTTA	3060
7498	Db		7557
		CGGTTTGGTGGAAAACCGTACAGCAAGCCATCTTATCTATCAAGGTGTCAAATCCTTTG	
3061	Qy	GGCGAACACCGGTACTGACTGTACCGCCCAAACACAGTCACTCATGGGGGCGGAAGGC	3120
7558	Db		7617
		GGCGAGAACCGGTGCTGACTATACCGCTTAATACAGTCACTCATGGGGGCGGAAGGC	
3121	Qy	AGAATTTCTCAAGTAGGAGCATCTCAATTTCTTGTATCAACGAGGGTCAATCATCTTCTCT	3180
7618	Db		7677
		AGAGTTCTCAAGTAGGTACATCTCAATTTCTTGTATCCAGGAGGGTCTTCATATTTCTCT	
3181	Qy	CCGCGTTATTTATCTTATGACAGTCAAGCAAAACAGCCACTCTTCATAGTCTCTTAT	3240
7678	Db		7737
		CCGCGTATTTATACCCCTATGACAGTCAAAACAAAAACGGCTACTCTCTTCATAGTCTCTAC	
3241	Qy	ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC	3300
7738	Db		7797
		ACATTCAATGCTTCACTCGGCCAGGTAGTGTCCCTTGCAGGCAATCAGCAAGTGCCCC	
3301	Qy	AACTCGTGTGTTACTCGAGTCTATACAGATCCCATATCCCCTAAATCTTTCTATAGAAACC	3358
7798	Db	AACTCATGTGTCACTGGAGTTATATACATGATCCGATCCCTTAAATCTTTCCATAGGAACC	7855

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 11:15:17 ; Search time 1694 Seconds
(without alignments)

11734.647 Million cell updates/sec

Title: US-10-800-256-1

Perfect score: 3358

Sequence: 1 acgggtagaagattctggat.....cctaattcttatagaacc 3358

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3358	100.0	3358	8	ACC47077
2	3353.2	99.9	15186	3	AZ44617
3	3353.2	99.9	15186	10	ADH71088
4	3353.2	99.9	15186	10	ADH62844
5	3240.4	96.5	5292	12	ADM78414
6	3196.4	95.2	3825	1	AN70261
7	2441.6	72.7	5291	12	ADM78418
8	1741.8	51.9	4177	2	AAQ68943
9	1741.8	51.9	4177	2	AAQ70570
10	1741.8	51.9	4177	2	AAQ48510
11	1741.8	51.9	4177	2	AAQ81147
12	1741.8	51.9	4177	3	AAZ49295
13	1741.8	51.9	4177	3	AAQ67862
14	1701.6	50.7	3570	6	ABK90556
15	1631.6	48.6	1662	2	AAT18203
16	1511	45.0	1907	2	AAQ98633
17	1511	45.0	1907	2	ADH23624
18	1509.4	44.9	1907	2	AAQ46678
19	1448	43.1	2176	2	AAQ13668
20	1427.2	42.5	1704	2	AAQ10060

21	1421.6	42.3	1734	2	AAT18205
22	1414.6	42.1	1812	4	AAC33148
23	1414	42.1	1662	12	ADP64628
24	1374.6	40.9	1685	6	AAL39864
25	1374.6	40.9	1685	10	ACC83258
26	1368.4	40.8	2521	2	AAV42534
27	1368.4	40.8	2521	12	ADM41154
28	1365.2	40.7	2521	2	AAT35875
29	1365.2	40.7	2521	2	AAT39330
30	1365.2	40.7	2521	2	AAT35921
31	1365.2	40.7	2521	2	AAV07021
32	1364	40.6	1734	2	AAT71745
33	1362.8	40.6	1682	2	AAV49342
34	1354.8	40.3	1784	1	AAN81290
35	1353.2	40.3	1764	2	AAQ20794
36	1290	38.4	1999	2	AAQ05549
37	1290	38.4	2000	1	AAAN1000
38	1238.2	36.9	1867	6	ABA99929
39	1196.8	35.6	1584	11	ADO55921
40	1193.6	35.5	1584	11	ADO55922
41	1192	35.5	1584	11	ADO55920
42	1160.8	34.6	1716	2	AAV49339
43	1090.4	32.5	1805	1	AAAN1032
44	1043.4	31.1	1648	11	ADO55933
45	1040.2	31.0	1648	11	ADO55936

ALIGNMENTS

RESULT 1

ACC47077

ID ACC47077 standard; DNA; 3358 BP.

XX ACC47077;

AC ACC47077;

DT 23-JUN-2003 (first entry)

XX Nucleotide sequence of F and HN genes of NDV strain HJ9.

DE NDV; lentogenic; oncolytic; fusion glycoprotein; F gene; HN gene;

KW haemagglutinin-neuraminidase; cytotstatic; gene therapy; cancer; ds.

XX Newcastle disease virus.

OS Newcastle disease virus.

PH Key Location/Qualifiers

FT CDS 47..3358

FT /*tag= a

FT /note= "contains internal stop codons"

XX WO2003022202-A2.

XX 20-MAR-2003.

XX 12-SEP-2002; 2002WO-IL000765.

XX 12-SEP-2001; 2001IL-00145397.

XX (YISS) YISSUM RES & DEV CO.

XX (OVCU-) OVCURE INC.

XX Zakay-Rones Z, Panet A, Irving C;

XX WPI; 2003-354498/33.

XX P-PSDB; ABR39678.

XX Clonal lentogenic oncolytic strain, particularly a HJ9 strain, of

XX Newcastle Disease Virus, useful for treating cancer, comprises a DNA

XX encoding a fusion gene and/or a hemagglutinin-neuraminidase gene.

XX Claim 1; Page 18-21; 51pp; English.

XX The invention relates to a clonal lentogenic oncolytic strain of

CC

1981 QY TTGATATCCGGATTGCAATCTTATTCTTACAGTAGTGACCTTGGCTATATCTGTAGCC 2040
1981 Db TTGATATCCGGATTGCAATCTTATTCTTACAGTAGTGACCTTGGCTATATCTGTAGCC 2040
2041 QY TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCGACTAGG 2100
2041 Db TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCGACTAGG 2100
2101 QY ATTTCAGGGCAGAAAGAAAGATTAATCTATCACTTGTGTTTCAATCAAGATGTAGTAGAT 2160
2101 Db ATTTCAGGGCAGAAAGAAAGATTAATCTATCACTTGTGTTTCAATCAAGATGTAGTAGAT 2160
2161 QY AGGATATATAGCAAGTGGCCCTGAGTCTCGTTGGCAATTTAAATACCTGAGACCA 2220
2161 Db AGGATATATAGCAAGTGGCCCTGAGTCTCGTTGGCAATTTAAATACCTGAGACCA 2220
2221 QY ATTATGAACGCAATAAATCTCTCTCTTATCAGATTAAATGAGCTGCAAAACAAGTGGG 2280
2221 Db ATTATGAACGCAATAAATCTCTCTCTTATCAGATTAAATGAGCTGCAAAACAAGTGGG 2280
2281 QY TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
2281 Db TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
2341 QY GATGATGCTAGTGTGATGTCACATCATCTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTT 2400
2341 Db GATGATGCTAGTGTGATGTCACATCATCTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTT 2400
2401 QY ATCCCGGGCTTACTACAGGATCAGTTGCTGCAATACCTCTATTTGACATCAGTGCT 2460
2401 Db ATCCCGGGCTTACTACAGGATCAGTTGCTGCAATACCTCTATTTGACATCAGTGCT 2460
2461 QY ACCATTACTCTACACCCATAATGTAATATGTTGCTGGATCAGAGATCACTCACATTC 2520
2461 Db ACCATTACTCTACACCCATAATGTAATATGTTGCTGGATCAGAGATCACTCACATTC 2520
2521 QY TATCAGTATTTAGACATTTGGTGTCTCGGACATCTGCAACAGGAGGGTATTTCTTTCT 2580
2521 Db TATCAGTATTTAGACATTTGGTGTCTCGGACATCTGCAACAGGAGGGTATTTCTTTCT 2580
2581 QY ACTCTGGCTTCCATCAACTCGAGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
2581 Db ACTCTGGCTTCCATCAACTCGAGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
2641 QY ACTCCCTGGTGTGTGATGATGCTGTCTCGAAAGTTCAGGAGACAGAGGAAGATTAT 2700
2641 Db ACTCCCTGGTGTGTGATGATGCTGTCTCGAAAGTTCAGGAGACAGAGGAAGATTAT 2700
2701 QY AACTCAGTGTCCCTACGCGGATGGTACATGGGAGGTTAGGGTTGACGCGGACGTACAC 2760
2701 Db AACTCAGTGTCCCTACGCGGATGGTACATGGGAGGTTAGGGTTGACGCGGACGTACAC 2760
2761 QY GAAAGGACCTAGATGTACAACTATTTCCGGGACTGGGTGGCCAACTACCCAGGAGTA 2820
2761 Db GAAAGGACCTAGATGTACAACTATTTCCGGGACTGGGTGGCCAACTACCCAGGAGTA 2820
2821 QY GGGGGTGGATCTTTTATTGACAGCGGCTATGTTCTCAGTCTACGAGGGTTAAAAACC 2880
2821 Db GGGGGTGGATCTTTTATTGACAGCGGCTATGTTCTCAGTCTACGAGGGTTAAAAACC 2880
2881 QY AATTACCCAGTACACTGTACAGGAAGGGAATATGTGATATACAAAGCGATACATGAC 2940
2881 Db AATTACCCAGTACACTGTACAGGAAGGGAATATGTGATATACAAAGCGATACATGAC 2940
2941 QY ACATGCCAGATGACCAAGTACAGATTTCGAATGCCAAGTCTTCGTATAGCCCTGGA 3000
2941 Db ACATGCCAGATGACCAAGTACAGATTTCGAATGCCAAGTCTTCGTATAGCCCTGGA 3000
3001 QY CGGTTTGGTGGAAACGATACAGCAGCTATCTTATCTCAAGGTGTCAACATCCTTA 3060
3001 Db CGGTTTGGTGGAAACGATACAGCAGCTATCTTATCTCAAGGTGTCAACATCCTTA 3060
3061 QY GGGGAGACCCGGTACTGTATACGCCCAACAGTCACTCATATGGGGGGCGAAGGC 3120

3061 Db GGGGAGACCCGGTACTGTATACGCCCAACAGTCACTCATATGGGGGGCGAAGGC 3120
3121 QY AGAATTCTCAGTAGGAGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTTCTCT 3180
3121 Db AGAATTCTCAGTAGGAGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTTCTCT 3180
3181 QY CCGCGTTTATATATCTTATGACAGTCAAGCAAAACAGCCACTCTTTCATAGTCTTAT 3240
3181 Db CCGCGTTTATATATCTTATGACAGTCAAGCAAAACAGCCACTCTTTCATAGTCTTAT 3240
3241 QY ACATTCAATCGCTTCACTCGGCCAGGTAGTATCCCTTGGCCAGGCTTCAGCAAGATGCC 3300
3241 Db ACATTCAATCGCTTCACTCGGCCAGGTAGTATCCCTTGGCCAGGCTTCAGCAAGATGCC 3300
3301 QY AACTCGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
3301 Db AACTCGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358

RESULT 2
AAZ44617
ID AAZ44617 standard; DNA; 15186 BP.
XX
AC AAZ44617;
XX
DT 07-APR-2000 (first entry)
XX
DE Newcastle disease virus LaSota genomic DNA.
XX
KW Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;
KW respiratory disease; gastrointestinal disease; poultry pathogen;
KW local immunity; ds.
XX
OS Newcastle disease virus.
XX
PH Key Location/Qualifiers
CDS 122..1591
FT /*tag= a
FT CDS 1887..3074
FT /*tag= b
FT CDS 3250..4384
FT /*tag= c
FT CDS 4544..6205
FT /*tag= d
FT CDS 6412..8145
FT /*tag= e
FT CDS 8381..14995
FT /*tag= f
XX
PN WO9966045-A1.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-NL000377.
XX
PR 19-JUN-1998; 98EP-00202054.
XX
PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
PI Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;
XX
DR WPI; 2000-106102/09.
XX
PT New avian paramyxovirus cDNA, useful for production of vaccine against
PT Newcastle disease virus.
XX
PS Disclosure; Fig 3; 115pp; English.
XX
CC This invention describes a novel avian-paramyxovirus cDNA (I) which
CC comprises a nucleic acid sequence corresponding to the 5' terminal end of
CC the genome of avian-paramyxovirus allowing the generation of an
CC infectious copy of avian-paramyxovirus. The cell line is useful for the

CC production of infectious lentogenic NDV (Newcastle Disease virus) without
CC the addition of exogenous proteolytic activity. Also it is possible to
CC generate a stable transfectant cell line that expresses the wild-type F
CC protein in the virus envelope therefore providing infectious particles,
CC useful in the form of a vaccine, especially against respiratory and/or
CC gastrointestinal diseases. NDV can be easily cultured to very high titers
CC in embryonated eggs. Mass culture of embryonated eggs is relatively
CC cheap. NDV vaccines are relatively stable and can be simply administered
CC by mass application methods e.g. drinking water or by spraying or by
CC aerosol formation. The natural route of infection is by the respiratory
CC and/or gastrointestinal tract which are also the major routes of
CC infection of many other poultry pathogens. NDV can induce local immunity
CC despite the presence of circulating maternal antibody. This sequence
CC represents the NDV strain LaSota genome DNA
XX
SQ Sequence 15186 BP; 4431 A; 3544 C; 3462 G; 3749 T; 0 U; 0 Other;

Query Match 99.9%; Score 3353.2; DB 3; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ACGGGTAGAAGATTCTCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
DB	4498	ACGGGTAGAAGATTCTCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
QY	61	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGGCGTGGCACTGAGTTG	120
DB	4558	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGGCGTGGCACTGAGTTG	4617
QY	121	CATCTGTCCGGAAACCTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTGGTTAC	180
DB	4618	CATCTGTCCGGAAACCTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTGGTTAC	4677
QY	181	AGGAGCAAGACCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
DB	4678	AGGAGCAAGACCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	4737
QY	241	CCTCCCGAATCTGCCAAGGATAAGAGGATGTGGGAAAGCCCTTGGATGCATACAA	300
DB	4738	CCTCCCGAATCTGCCAAGGATAAGAGGATGTGGGAAAGCCCTTGGATGCATACAA	4797
QY	301	CAGGACATTGACCACTTTGCTACCCCTTTGGTGAATCTATCCGTAGGATACAAGATC	360
DB	4798	CAGGACATTGACCACTTTGCTACCCCTTTGGTGAATCTATCCGTAGGATACAAGATC	4857
QY	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCCTTATAGGCGCCATTTATGGCGGTG	420
DB	4858	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCCTTATAGGCGCCATTTATGGCGGTG	4917
QY	421	GGCTCTTGGGTTGCAACTGCCGCAAAATAACAGCGCGCCAGCTCTGTATACAAGCCAA	480
DB	4918	GGCTCTTGGGTTGCAACTGCCGCAAAATAACAGCGCGCCAGCTCTGTATACAAGCCAA	4977
QY	481	ACAAATGCTGCCAATCTCCGACTTAAAGAGAGANTTGGCGCAACCAATGAGGCTGT	540
DB	4978	ACAAATGCTGCCAATCTCCGACTTAAAGAGAGANTTGGCGCAACCAATGAGGCTGT	5037
QY	541	GCATGAGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAGAGTGCAGAGTT	600
DB	5038	GCATGAGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAGAGTGCAGAGTT	5097
QY	601	TGTTAATGACCAATTTAATAAAGACGCTCAGGAATTAGCTGCATCAAAATTCACAGCA	660
DB	5098	TGTTAATGACCAATTTAATAAAGACGCTCAGGAATTAGCTGCATCAAAATTCACAGCA	5157
QY	661	AGTTGGTGTAGACTCAACTGTACCTTACCGAATGACTACAGTATTCGGACCAAAAT	720
DB	5158	AGTTGGTGTAGACTCAACTGTACCTTACCGAATGACTACAGTATTCGGACCAAAAT	5217
QY	721	CACCTCACCTGCTTTAAACAGCTGACTATTTCAGGCACCTTTACAATCTAGCTGGTGA	780
DB	5218	CACCTCACCTGCTTTAAACAGCTGACTATTTCAGGCACCTTTACAATCTAGCTGGTGA	5277

QY	781	TATGGATTACTTATCTAAGTTAGGTGTAGGAAACAATCAACTCAGCTCATTAATCGG	840
DB	5278	TATGGATTACTTATCTAAGTTAGGTGTAGGAAACAATCAACTCAGCTCATTAATCGG	5337
QY	841	TAGCGGCTTAATCACCAGGTAAACCTTATCTATAGACTCAGACTCAACTCTTGGGTAT	900
DB	5338	TAGCGGCTTAATCACCAGGTAAACCTTATCTATAGACTCAGACTCAACTCTTGGGTAT	5397
QY	901	ACAGGTAACTCTACCTTTCAGTGGGAAACCTTAATAATATATGCGTGCCACCTTACCTT	960
DB	5398	ACAGGTAACTCTACCTTTCAGTGGGAAACCTTAATAATATATGCGTGCCACCTTACCTT	5457
QY	961	CTTATCCGTAAGCACCAACAGGGGATTTGCCCTGGCACTTTGCCAAAAGTGGTGACACA	1020
DB	5458	CTTATCCGTAAGCACCAACAGGGGATTTGCCCTGGCACTTTGCCAAAAGTGGTGACACA	5517
QY	1021	GGTGGGTTCTGTGATAGAGAACTTGACACCTCATACTGTATAGAACTGACTTAGATTT	1080
DB	5518	GGTGGGTTCTGTGATAGAGAACTTGACACCTCATACTGTATAGAACTGACTTAGATTT	5577
QY	1081	ATATTGTCAAGAATAAGTAAACGTTCCCTATGTCCCTGGTATTATTCTCTGTGTAGCGG	1140
DB	5578	ATATTGTCAAGAATAAGTAAACGTTCCCTATGTCCCTGGTATTATTCTCTGTGTAGCGG	5637
QY	1141	CAATACGTCCGGCTGTATGTACTCAAAGACCGAAGCGCACCTTACTACACCATACATGAC	1200
DB	5638	CAATACGTCCGGCTGTATGTACTCAAAGACCGAAGCGCACCTTACTACACCATACATGAC	5697
QY	1201	TATCAAAGGTTGAGTCAATGCCAATCTGCAAGATGACAAACATGTAGATGTGTAAACCCCCC	1260
DB	5698	TATCAAAGGTTGAGTCAATGCCAATCTGCAAGATGACAAACATGTAGATGTGTAAACCCCCC	5757
QY	1261	GGGTATCATATCGCAAAACCTATGGGAAGCGGTCTCTTAATAGATAAAACAATCATGCAA	1320
DB	5758	GGGTATCATATCGCAAAACCTATGGGAAGCGGTCTCTTAATAGATAAAACAATCATGCAA	5817
QY	1321	TGTTTTATCTTTAGGCGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
DB	5818	TGTTTTATCTTTAGGCGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	5877
QY	1381	GAAGAAATCTCAATACAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
DB	5878	GAAGAAATCTCAATACAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	5937
QY	1441	TGAGCTTTGGGAATGTCAACCACTCGATCAGTAAATGCTTTTGAATAAGTTAGAGAAAGCAA	1500
DB	5938	TGAGCTTTGGGAATGTCAACCACTCGATCAGTAAATGCTTTTGAATAAGTTAGAGAAAGCAA	5997
QY	1501	CAGAAAACCTAGACAAAGTCAATGTCAAACCTAGCTAGCACATCTGCTCTCATTAACCTATAT	1560
DB	5998	CAGAAAACCTAGACAAAGTCAATGTCAAACCTAGCTAGCACATCTGCTCTCATTAACCTATAT	6057
QY	1561	CGTTTTGACTATCATATCTCTTGTGTTTGGTATACCTTAGCTGATTTCTAGCATGTACCT	1620
DB	6058	CGTTTTGACTATCATATCTCTTGTGTTTGGTATACCTTAGCTGATTTCTAGCATGTACCT	6117
QY	1621	AATGTACAAAGCAAAAGCGCAACAAAACCTTTATTTGCTTGGGAATAAATACTCTAGA	1680
DB	6118	AATGTACAAAGCAAAAGCGCAACAAAACCTTTATTTGCTTGGGAATAAATACTCTAGA	6177
QY	1681	TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGAAACGAGGTTTCCCTAATAG	1740
DB	6178	TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGAAACGAGGTTTCCCTAATAG	6237
QY	1741	TAAATTTGTGAAGGTTCTGTGAGTGTCTGCTGAGTTGAGAGGTTAGAAAAAATACCCGT	1800
DB	6238	TAAATTTGTGAAGGTTCTGTGAGTGTCTGCTGAGTTGAGAGGTTAGAAAAAATACCCGT	6297
QY	1801	TGTAGATGACCAAGGACCATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTCG	1860
DB	6298	TGTAGATGACCAAGGACCATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTCG	6357
QY	1861	GAGCCAGGCTTCACAAACCTCCGTTCTACCGCTTCCACCGAACACAGTCTCAATCATGGAC	1920

CC stimulates a protective immune response of a viral vaccine against the
CC avian virus. VAF is useful as a vaccine against Marek's disease virus
CC (MDV), infectious disease virus (IBDV), Newcastle disease virus
CC (NDV), infectious bronchitis virus (IBV), fowlpox virus (FPV), infectious
CC laryngotracheitis virus (ILT), avian encephalomyelitis virus (AEV),
CC avian leukosis virus (ALV), avian parainfluenza virus (APV), duck
CC hepatitis virus (DHV) and hemorrhagic enteritis virus (HEV) in chicken.
CC The present sequence is NDV HN gene.
XX
SQ Sequence 15186 BP; 4431 A; 3542 C; 3464 G; 3749 T; 0 U; 0 Other;

Query Match 99.9%; Score 3353.2; DB 10; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGGGTAGAGATTCTCGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 60
DB 4498 ACGGGTAGAGATTCTCGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 4557

QY 61 TTCTACCAAGAACCCAGCACCCTATGATGCTGACTATATCCGGGTTCGCGTGGCACTGAGTTG 120
DB 4558 TTCTACCAAGAACCCAGCACCCTATGATGCTGACTATATCCGGGTTCGCGTGGCACTGAGTTG 4617

QY 121 CATCTGTCGGGCAAACTCCATTTGATGGCAGGCTCTTGGCAGCTGCAGGAATTTGGTTAC 180
DB 4618 CATCTGTCGGGCAAACTCCATTTGATGGCAGGCTCTTGGCAGCTGCAGGAATTTGGTTAC 4677

QY 181 AGGAGACAAAGCCGTCAACATATACCTCATCCAGCAGGATCAATCATAGTTAAGCT 240
DB 4678 AGGAGACAAAGCCGTCAACATATACCTCATCCAGCAGGATCAATCATAGTTAAGCT 4737

QY 241 CCTCCGAAATCTGCCAAGGATAGAGGAGCATGTGCGAAAGCCCCCTTGGATGCATACAA 300
DB 4738 CCTCCGAAATCTGCCAAGGATAGAGGAGCATGTGCGAAAGCCCCCTTGGATGCATACAA 4797

QY 301 CAGACATTTGACCACTTTGCTCACCCCCTTTGFGACTCTATCCGTTAGATACAAAGTTC 360
DB 4798 CAGACATTTGACCACTTTGCTCACCCCCTTTGFGACTCTATCCGTTAGATACAAAGTTC 4857

QY 361 TGTGACTACATCTGGAGGGGGGACAGGGCGCCTTATAGGCGCCATTTAGCGCGTGT 420
DB 4858 TGTGACTACATCTGGAGGGGGGACAGGGCGCCTTATAGGCGCCATTTAGCGCGTGT 4917

QY 421 GGCTCTTTGGGGTTCGAACCTGCGCACAAATAACAGCGCGCGCAGCTCTGATACAAAGCAA 480
DB 4918 GGCTCTTTGGGGTTCGAACCTGCGCACAAATAACAGCGCGCGCAGCTCTGATACAAAGCAA 4977

QY 481 ACAAATGCTGCCAACAATCTCCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT 540
DB 4978 ACAAATGCTGCCAACAATCTCCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT 5037

QY 541 GCATGAGGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGCGAGCTT 600
DB 5038 GCATGAGGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGCGAGCTT 5097

QY 601 TGTAAATGACCAATTTAAATAAACAGCTCAGGAATTAGACTGCAATCAAAATTCGACAGCA 660
DB 5098 TGTAAATGACCAATTTAAATAAACAGCTCAGGAATTAGACTGCAATCAAAATTCGACAGCA 5157

QY 661 AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCACAAT 720
DB 5158 AGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCACAAT 5217

QY 721 CACTTCACCTGCTTTAAACAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGAAA 780
DB 5218 CACTTCACCTGCTTTAAACAGCTGACTATTCAGGCACTTTACATCTAGCTGGTGAAA 5277

QY 781 TATGGAATTAATTTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 840
DB 5278 TATGGAATTAATTTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 5337

QY 841 TAGCGGCTTAATCAACCGGTAAACCTTATTCATACGACTCAAGACTCAATCTTTGGGTAT 900
DB

DB 5338 TAGCGGCTTAATCAACCGGTAAACCTTATTTCTATACGACTCACAGACTCAACTCTTGGGTAT 5397
QY 901 ACAGGTAACTCTACCTTTCACTGGGAACTTAATAATATATCGTGGCCACCTACTTGGAAAC 960
DB 5398 ACAGGTAACTCTACCTTTCACTGGGAACTTAATAATATATCGTGGCCACCTACTTGGAAAC 5457
QY 961 CTTATCCGTTAAGCAACACAGGGGATTTGCTTCGGCAGCTTGTCCCAAAAAGTGGTGACACA 1020
DB 5458 CTTATCCGTTAAGCAACACAGGGGATTTGCTTCGGCAGCTTGTCCCAAAAAGTGGTGACACA 5517
QY 1021 GGTTCGGTCTCTGATAGAGAACTTGACACCTCATACTATATAGAACTGACTTAGATTT 1080
DB 5518 GGTTCGGTCTCTGATAGAGAACTTGACACCTCATACTATATAGAACTGACTTAGATTT 5577
QY 1081 ATATTCTCAAGAATAAGTAAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAACGG 1140
DB 5578 ATATTCTCAAGAATAAGTAAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAACGG 5637
QY 1141 CAATACGTCGGCTGTATGTATCTCAAAAGCCGAAAGCGCACTTATACACCATATATGAC 1200
DB 5638 CAATACGTCGGCTGTATGTATCTCAAAAGCCGAAAGCGCACTTATACACCATATATGAC 5697
QY 1201 TATCAAAAGTTCACTCATCGCCAACTGCAAGATGACAACTGTAGATGTGTAACCCCCC 1260
DB 5698 TATCAAAAGTTCACTCATCGCCAACTGCAAGATGACAACTGTAGATGTGTAACCCCCC 5757
QY 1261 GGGTATCATATCGCAAACTATGGAGAGCGGTGTCTTAATAGATAAAACAATCATGCA 1320
DB 5758 GGGTATCATATCGCAAACTATGGAGAGCGGTGTCTTAATAGATAAAACAATCATGCA 5817
QY 1321 TGTATTATCTTTAGGGGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380
DB 5818 TGTATTATCTTTAGGGGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877
QY 1381 GAAGATAATCTCAATACAGATTCTCAAGTAAATAACAGGCAATCTTGATATCTCAAC 1440
DB 5878 GAAGATAATCTCAATACAGATTCTCAAGTAAATAACAGGCAATCTTGATATCTCAAC 5937
QY 1441 TGAGCTTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTGAATAGTTAGAGGAAAGCAA 1500
DB 5938 TGAGCTTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTGAATAGTTAGAGGAAAGCAA 5997
QY 1501 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCTCTCATTTACCTATAT 1560
DB 5998 CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCTCTCATTTACCTATAT 6057
QY 1561 CGTTTGTGACTATCATATCTTTGTTTGGTATACCTTAGCCTGATTTAGCATGCTACCT 1620
DB 6058 CGTTTGTGACTATCATATCTTTGTTTGGTATACCTTAGCCTGATTTAGCATGCTACCT 6117
QY 1621 AATGTACAAAGCAAGGGCGCAACAAAAACCTTTATTTATGGCTTGGGAATAATACTCTAGA 1680
DB 6118 AATGTACAAAGCAAGGGCGCAACAAAAACCTTTATTTATGGCTTGGGAATAATACTCTAGA 6177
QY 1681 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG 1740
DB 6178 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG 6237
QY 1741 TAAATTTGTGAAAAGTTCTTGTTAGTCTCTGAGTTCAGTTCAGAGAGTTAAGAAAAAAGTACCGGT 1800
DB 6238 TAAATTTGTGAAAAGTTCTTGTTAGTCTCTGAGTTCAGTTCAGAGAGTTAAGAAAAAAGTACCGGT 6297
QY 1801 TGTAGATGACCAAGGACGATATACCGGTAGAACCGTGAAGAGAGGGCGCCCTCAATTCG 1860
DB 6298 TGTAGATGACCAAGGACGATATACCGGTAGAACCGTGAAGAGAGGGCGCCCTCAATTCG 6357
QY 1861 GAGCCAGGCTTCAACCTTCGGTTTACCGCTTACCGCAACACAGTCTCTCAATCATGGAC 1920
DB 6358 GAGCCAGGCTTCAACACCTTCGGTTTACCGCTTACCGCAACACAGTCTCTCAATCATGGAC 6417
QY 1921 CGCGCGCTTAGCCCAAGTTGCGTTAGAGATGATGAAGAGAGGCAAAAAATACATCGGC 1980
DB 6418 CGCGCGCTTAGCCCAAGTTGCGTTAGAGATGATGAAGAGAGGCAAAAAATACATCGGC 6477

Qy	1	ACGGGTAGAGATTCTGTGATCCCGTTGGGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	4498	ACGGGTAGAGATTCTGTGATCCCGTTGGGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
Qy	61	TTCTACCAAGAACCCAGCCTATGATGCTGACTATCCGGTTGGCGTGGCACTGAGTTG	120
Db	4558	TTCTACCAAGAACCCAGCCTATGATGCTGACTATCCGGTTGGCGTGGCACTGAGTTG	4617
Qy	121	CATCTGTCCGGCAAACTCCAATTGATGGCAGGCCCTCTTGCAGCTGCGAGAAATTGGGTTAC	180
Db	4618	CACTCTGCCGCAAACTCCAATTGATGGCAGGCCCTCTTGCAGCTGCGAGAAATTGGGTTAC	4677
Qy	181	AGGAGACAAAGCCGCTCAACATATACACCTCATCCACAGCAGGATCAATCATAGTTAAGCT	240
Db	4678	AGGAGACAAAGCCGCTCAACATATACACCTCATCCACAGCAGGATCAATCATAGTTAAGCT	4737
Qy	241	CCTCCCGAATCTGCCAAGATAGGAGGCATGTGCGAAAGCCCCCTTGGATGCATACAA	300
Db	4738	CCTCCCGAATCTGCCAAGATAGGAGGCATGTGCGAAAGCCCCCTTGGATGCATACAA	4797
Qy	301	CAGGACATTGACCACTTTGTCTACCCCCCTTTGGTGACTCTATCCGTAGGATACAAAGTGC	360
Db	4798	CAGGACATTGACCACTTTGTCTACCCCCCTTTGGTGACTCTATCCGTAGGATACAAAGTGC	4857
Qy	361	TGTGACTACATCTGGAGGGGGAGACAGGGGCGCCTTTATAGGCGCCATTATTGGCGGTGT	420
Db	4858	TGTGACTACATCTGGAGGGGGAGACAGGGGCGCCTTTATAGGCGCCATTATTGGCGGTGT	4917
Qy	421	GGCTCTTGGGGTTGCAACTGCGGCACAAATAACAGCGGCGCGAGCTCTGATACAGCCAA	480
Db	4918	GGCTCTTGGGGTTGCAACTGCGGCACAAATAACAGCGGCGCGAGCTCTGATACAGCCAA	4977
Qy	481	ACAAATGCTGCCAAATCTCCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT	540
Db	4978	ACAAATGCTGCCAAATCTCCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT	5037
Qy	541	GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT	600
Db	5038	GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT	5097
Qy	601	TGTTAATGACCAATTTAATAAACAGCTCAGGAATTAGACTGCATCAAAATTGCAACGA	660
Db	5098	TGTTAATGACCAATTTAATAAACAGCTCAGGAATTAGACTGCATCAAAATTGCAACGA	5157
Qy	661	AGTTGGTGTAGAGCTCAACTGTACCTTAACCGAATTGACTACAGTATTTCGGACCAAAAT	720
Db	5158	AGTTGGTGTAGAGCTCAACTGTACCTTAACCGAATTGACTACAGTATTTCGGACCAAAAT	5217
Qy	721	CACCTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTACAATCTAGCTGGTGGAAA	780
Db	5218	CACCTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTACAATCTAGCTGGTGGAAA	5277
Qy	781	TATGGATTACTTATGACTAAGTTAGTTAGTTAGGGAAACAATCAACTCAGCTCATTAATCGG	840
Db	5278	TATGGATTACTTATGACTAAGTTAGTTAGTTAGGGAAACAATCAACTCAGCTCATTAATCGG	5337
Qy	841	TAGCGGCTTAATCACCGGTAAACCTATTCTATAGGACTCACAGACTCAACTCTTTGGGTAT	900
Db	5338	TAGCGGCTTAATCACCGGTAAACCTATTCTATAGGACTCACAGACTCAACTCTTTGGGTAT	5397
Qy	901	ACAGGTAACTCTACCTTTCAGTCGGGAACTTAAATAATATATCGTGCCACCTTCTGGAAAC	960
Db	5398	ACAGGTAACTCTACCTTTCAGTCGGGAACTTAAATAATATATCGTGCCACCTTCTGGAAAC	5457
Qy	961	CTTATCCGTAAAGCAACAGGGGATTTCCTCGGCATCTTGCCCAAAAGTGTGACACA	1020
Db	5458	CTTATCCGTAAAGCAACAGGGGATTTCCTCGGCATCTTGCCCAAAAGTGTGACACA	5517
Qy	1021	GGTCGGTTCGTGATAGAGAACTTGACACCTCATCTGATATAGAACTGACATTAGATTT	1080
Db	5518	GGTCGGTTCGTGATAGAGAACTTGACACCTCATCTGATATAGAACTGACATTAGATTT	5577
Qy	1081	ATATTGTACAGAATAGTAACGTTCCCTATGTCCCTGGTATTTATTTCTCTGTGAGCGG	1140

Db	5578	ATATTGTACAGAATAGTAACGTTCCCTATGTCCCTGGTATTTATTTCTCTGCTTGAGCGG	5637
Qy	1141	CAATACGTCCGCCCTGTATGTACTCAAGACCGAAGCGGCACTTACTACACCATACATGAC	1200
Db	5638	CAATACGTCCGCCCTGTATGTACTCAAGACCGAAGCGGCACTTACTACACCATACATGAC	5697
Qy	1201	TATCAAAAGGTTTCAGTTCATGCCCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC	1260
Db	5698	TATCAAAAGGTTTCAGTTCATGCCCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC	5757
Qy	1261	GGGTATCATATCGCAAAAATATGGAGAACCGGTGTCTTAATAGATAAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAAAATATGGAGAACCGGTGTCTTAATAGATAAAACAATCATGCAA	5817
Qy	1321	TGTTTTATCTTTAGGCGGGATTAACCTTTAAGGCTCAGTGGGGAAATCGATGTAACTTATCA	1380
Db	5818	TGTTTTATCTTTAGGCGGGATTAACCTTTAAGGCTCAGTGGGGAAATCGATGTAACTTATCA	5877
Qy	1381	GAAGAATATCTCAATACAAAGATTCTCAAGTAATAAACAAGGCAATCTTTGATATCTCAAC	1440
Db	5878	GAAGAATATCTCAATACAAAGATTCTCAAGTAATAAACAAGGCAATCTTTGATATCTCAAC	5937
Qy	1441	TGAGCTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTGAAATAAGTTAGAGGAAAGCAA	1500
Db	5938	TGAGCTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTGAAATAAGTTAGAGGAAAGCAA	5997
Qy	1501	CAGAAACTAGACAAAGTCAATGTCAAACTGACTAGACACATCGCTCTCATTTACCTATAT	1560
Db	5998	CAGAAACTAGACAAAGTCAATGTCAAACTGACTAGACACATCGCTCTCATTTACCTATAT	6057
Qy	1561	CGTTTTGACTATCATATCTCTTGTGTTTGGTATPACTTAGCCTGATTCTAGCATGCTACCT	1620
Db	6058	CGTTTTGACTATCATATCTCTTGTGTTTGGTATPACTTAGCCTGATTCTAGCATGCTACCT	6117
Qy	1621	AATGTACAGCAAAAGGCGCAACAAAAGACCTTATTATGGCTTGGGAATAAATACTCTAGA	1680
Db	6118	AATGTACAGCAAAAGGCGCAACAAAAGACCTTATTATGGCTTGGGAATAAATACTCTAGA	6177
Qy	1681	TCAGATGAGGCGCACTACAAAATGTGAACAGATGAGGACGAAAGGTTCCCTAATAG	1740
Db	6178	TCAGATGAGGCGCACTACAAAATGTGAACAGATGAGGACGAAAGGTTCCCTAATAG	6237
Qy	1741	TAATTTGTGTGAAAGTTCTGTGTAGTCTGTGAGTTCAGAGAGTTTAAGAAAAAATACCGGT	1800
Db	6238	TAATTTGTGTGAAAGTTCTGTGTAGTCTGTGAGTTCAGAGAGTTTAAGAAAAAATACCGGT	6297
Qy	1801	TGTAGATGACCAAAAGGACGATATACGGGTAGAAACGGTAAAGAGAGGCGCCCTCAATTGC	1860
Db	6298	TGTAGATGACCAAAAGGACGATATACGGGTAGAAACGGTAAAGAGAGGCGCCCTCAATTGC	6357
Qy	1861	GAGCCAGGCTTCACAACTCCGTTCTACCGCTTCACGCAACAGTCCCTCAATCATGGAC	1920
Db	6358	GAGCCAGGCTTCACAACTCCGTTCTACCGCTTCACGCAACAGTCCCTCAATCATGGAC	6417
Qy	1921	CGCGCGTTAGCCCAAGTTCGGTTAGAGAATGATGAAGAGAGAGCAAAAAATACATGGCGC	1980
Db	6418	CGCGCGTTAGCCCAAGTTCGGTTAGAGAATGATGAAGAGAGAGCAAAAAATACATGGCGC	6477
Qy	1981	TTGATATTCCGGAATTGCAATCTTATTCTTAACAGTAGTGACCTTGGCTATATCTGTAGCC	2040
Db	6478	TTGATATTCCGGAATTGCAATCTTATTCTTAACAGTAGTGACCTTGGCTATATCTGTAGCC	6537
Qy	2041	TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATCCGACTAGG	2100
Db	6538	TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTGTAGGCATCCGACTAGG	6597
Qy	2101	ATTTCCAGGGCAGAGAAAAAGATTACATCTACATTTGGTTCCAAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGGCAGAGAAAAAGATTACATCTACATTTGGTTCCAAATCAAGATGTAGTAGAT	6657
Qy	2161	AGGATATATAAGCAAGTGGCCCTTGGTCTCCGTTGGCAATGTTGTTAAATCTGAGACACA	2220

Db 6658 AGGATATATAAGCAAGTGGCCCTTGAGTCTCGGTTGGCATTTGTTAAATCTAGACACACA 6717
Qy 2221 ATTATGAACCAATAACATCTCTCTCTATCAGATTAATGAGCTGCGAAACAAACAGTGGG 2280
Db 6718 ATTATGAACCAATAACATCTCTCTCTATCAGATTAATGAGCTGCGAAACAAACAGTGGG 6777
Qy 2281 TGGGGGGCACCTATCCATGACCCAGATATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 6778 TGGGGGGCACCTATCCATGACCCAGATATATAGGGGGATAGGCAAGAACTCATTTGTA 6837
Qy 2341 GATGATGCTAGTGTGATGTCATCATCTCTATCCCTCTGCAATTCGAAGCAATCTCAATTTT 2400
Db 6838 GATGATGCTAGTGTGATGTCATCATCTCTATCCCTCTGCAATTCGAAGCAATCTCAATTTT 6897
Qy 2401 ATCCGGGGCTACTACAGATCAGGTGCACTCGAATACCCCTCATTTGACATGAGTGT 2460
Db 6898 ATCCGGGGCTACTACAGATCAGGTGCACTCGAATACCCCTCATTTGACATGAGTGT 6957
Qy 2461 ACCATTACTGCTACACCCCAATGTAATATTGCTGTGATGTCAGATCAGATCAGATTC 2520
Db 6958 ACCATTACTGCTACACCCCAATGTAATATTGCTGTGATGTCAGATCAGATCAGATTC 7017
Qy 2521 TATCAGTATTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGGTATCTTTCT 2580
Db 7018 TATCAGTATTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGGTATCTTTCT 7077
Qy 2581 ACTTCGGTTCATCAACTCGGACACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
Db 7078 ACTTCGGTTCATCAACTCGGACACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 7137
Qy 2641 ACTCCCTGGTGTGATGCTGTCTGCGAAGTCCAGGACAGAGGAAGAGATAT 2700
Db 7138 ACTCCCTGGTGTGATGCTGTCTGCGAAGTCCAGGACAGAGGAAGAGATAT 7197
Qy 2701 AACTCAGCTGCTCCATCGCGATGCTCATCGGAGGTTAGGGTTCGACGGCCAGTACCAC 2760
Db 7198 AACTCAGCTGCTCCATCGCGATGCTCATCGGAGGTTAGGGTTCGACGGCCAGTACCAC 7257
Qy 2761 GAAAGGACCTAGATGTACAAACATTTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Db 7258 GAAAGGACCTAGATGTACAAACATTTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 7317
Qy 2821 GGGGGTGATCTTTATTGACAGCGCGGTATGGTTCTCAGTCTACGAGGGTTAAACCC 2880
Db 7318 GGGGGTGATCTTTATTGACAGCGCGGTATGGTTCTCAGTCTACGAGGGTTAAACCC 7377
Qy 2881 AATTCAACCCAGTACACTGACAGAGGGAATATGTGATATACAGCGATACAATGAC 2940
Db 7378 AATTCAACCCAGTACACTGACAGAGGGAATATGTGATATACAGCGATACAATGAC 7437
Qy 2941 ACATGCCCAGATGACAGACTACAGATTCGAATGGCCAGTCTTCGTATAGCCCTGGA 3000
Db 7438 ACATGCCCAGATGACAGACTACAGATTCGAATGGCCAGTCTTCGTATAGCCCTGGA 7497
Qy 3001 CGGTTTGGTGGAAACCGATACAGAGCTATCTTATCTATCAAGGTTCAACATCCTTA 3060
Db 7498 CGGTTTGGTGGAAACCGATACAGAGCTATCTTATCTATCAAGGTTCAACATCCTTA 7557
Qy 3061 GGGCAAGACCGGTACTGACTGTACCGCCCAACACAGTACACTCATGGGGCCGAGGC 3120
Db 7558 GGGCAAGACCGGTACTGACTGTACCGCCCAACACAGTACACTCATGGGGCCGAGGC 7617
Qy 3121 AGAATTCCTCAGTAGGACATCTCATTTCTGTATCAACGAGGTCATCATCTCTCT 3180
Db 7618 AGAATTCCTCAGTAGGACATCTCATTTCTGTATCAACGAGGTCATCATCTCTCT 7677
Qy 3181 CCGCGTTATTATCTCCTATGACAGTACAGCAACAAAACAGCCACTCTTCATAGTCCTTAT 3240
Db 7678 CCGCGTTATTATCTCCTATGACAGTACAGCAACAAAACAGCCACTCTTCATAGTCCTTAT 7737
Qy 3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTGCGAGGTTGACAGAGATGCC 3300
Db 7738 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTGCGAGGTTGACAGAGATGCC 7797

Qy 3301 AACTCGTGTCTACTGAGTCTATACAGATCCATATCCCTCAATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTCTACTGAGTCTATACAGATCCATATCCCTCAATCTTCTATAGAAACC 7855

RESULT 5

ADM78414
ID ADM78414 standard; cDNA; 5292 BP.
XX
AC ADM78414;
XX
DT 03-JUN-2004 (first entry)
XX
DE Newcastle disease virus recombinant cDNA #10.
XX
KW Newcastle disease virus; T7 RNA polymerase; HEP-2 cell; influenza virus;
KW infectious bursal disease virus; rotavirus; infectious bronchitis virus;
KW chicken anaemia virus; Marek's disease virus; avian Leukosis virus;
KW avian adenovirus; avian pneumovirus;
KW severe acute respiratory syndrome-causing virus; SARS;
KW human respiratory syncytial virus; human immunodeficiency virus;
KW hepatitis virus; measles virus; mumps virus; antiviral; ss.
XX
OS Newcastle disease virus.
XX
FN US2003224017-A1.
XX
PD 04-DEC-2003.
XX
PF 19-MAY-2003; 2003US-00440419.
XX
PR 05-MAY-2000; 2000WO-US006700.
PR 06-MAR-2002; 2002US-00926431.
PR 17-MAY-2002; 2002US-0381462P.
XX
PA (SAMA/) SAMAL S K.
PA (HUAN/) HUANG Z.
XX
PI Samal SK, Huang Z;
XX
PI WPI; 2004-051891/05.
XX
DR
XX
PT Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN,
PT L genes and foreign nucleotide complex inserted before NP gene, between
PT P, M genes and/or between HN, L genes, useful for producing vaccine
PT vector.
XX
PS Example 3; Page 12-14; 41pp; English.
XX
CC The invention relates to an antigenomic RNA of Newcastle disease virus
CC having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign
CC nucleotide complexes inserted between genes. The invention also relates
CC to cDNA related to the RNA, a plasmid comprising the cDNA, a cell
CC comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a
CC recombinant Newcastle disease virus comprising the RNA. The RNA is useful
CC for producing a recombinant Newcastle disease virus by providing cells
CC capable of synthesizing T7 RNA polymerase, transfecting the cells with a
CC plasmid comprising cDNA or a protein of interest to obtain transfected
CC cells in a medium and isolating Newcastle disease virus from a
CC supernatant of the medium, where the cells capable synthesizing T7 RNA
CC polymerase are from a cell line expressing T7 RNA polymerase or plant
CC cells, mammalian cells, avian cells or HEP-2 cells infected with a
CC vaccinia virus that can synthesize T7 RNA polymerase. The recombinant
CC virus is useful for vaccinating an avian animal against Newcastle disease
CC or an avian pathogen chosen from influenza virus, infectious bursal
CC disease virus, rotavirus, infectious bronchitis virus, chicken anaemia
CC virus, Marek's disease virus, avian Leukosis virus, avian adenovirus and
CC avian pneumovirus, where the avian animal is in need of the immunisation,
CC which involves administering the recombinant virus to the avian animal,
CC where the open reading frame of the foreign gene encodes an immunogenic
CC protein of the avian pathogen against which the avian animal is
CC immunized. The recombinant virus is also useful for immunising a mammal

CC	against a non-avian pathogen such as severe acute respiratory syndrome-
CC	causing virus (SARS virus), human respiratory syncytial virus, human
CC	immunodeficiency virus, hepatitis virus, measles virus or mumps virus.
CC	This sequence represents Newcastle disease virus recombinant cDNA of the
CC	invention.
XX	
SQ	Sequence 5292 BP; 1574 A; 1207 C; 1186 G; 1324 T; 0 U; 1 Other;
	Query Match 96.5%; Score 3240.4; DB 12; Length 5292;
	Best Local Similarity 99.7%; Pred. No. 0;
	Matches 3267; Conservative 1; Mismatches 8; Indels 2; Gaps 2;
Qy	82 TATGATCGTCACTATCCGGTGGCTGGCGCTGACAGTTCAGTTCCTGCGGCAAACTCCAT 141
Db	1 TATGATCGTCACTATCCGGTGGCTGGCTGACTGAGTTGCATCTGTCCGGCAAACTCCAT 60
Qy	142 TGAATGGCAGGCTTTGCAGCTGCAGGAATGTGGTTACAGGAGACAAAGCCGTCAACAT 201
Db	61 TGAATGGCAGGCTTTGCAGCTGCAGGAATGTGGTTACAGGAGACAAAGCCGTCAACAT 120
Qy	202 ATACACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCCGNAATCGCCCAAGGA 261
Db	121 ATACACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCCGAATCTGCCCAAGGA 180
Qy	262 TAAGGAGGCATGTGCGAAAGCCCTTGGATGCATACAAACAGACATTTGACCACTTTGCT 321
Db	181 TAAGGAGGCATGTGCGAAAGCCCTTGGATGCATACAAACAGACATTTGACCACTTTGCT 240
Qy	322 CACCCCTTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGGAGGGG 381
Db	241 CACCCCTTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGGAGGGG 300
Qy	382 GAGACAGGGGGCTTATAGCGGCATTTATGGCGGTGTGGCTCTTGGGGTTGCAACTGC 441
Db	301 GAGACAGGGGGCTTATAGCGGCATTTATGGCGGTGTGGCTCTTGGGGTTGCAACTGC 360
Qy	442 CGCAAAATTAACAGCGCGCGAGCTCTGATACAAGCCAAACAAATGCTGCCAACATCCT 501
Db	361 CGCAAAATTAACAGCGCGCGAGCTCTGATACAAGCCAAACAAATGCTGCCAACATCCT 420
Qy	502 CCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGTGCATGAGGTCTACTGACGGATT 561
Db	421 CCGACTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGTGCATGAGGTCTACTGACGGATT 480
Qy	562 ATCCCACTAGCAGTGCAGTTGGGAAGATGCAGCAGTTTGTAAATGACCAATTTAATAA 621
Db	481 ATCCCACTAGCAGTGCAGTTGGGAAGATGCAGCAGTTTGTAAATGACCAATTTAATAA 540
Qy	622 AACAGCTCAGGAATTAGACTGCATCAAAATTTGCACGAAGTTGGTGTAGAGCTCAACCT 681
Db	541 AACAGCTCAGGAATTAGACTGCATCAAAATTTGCACGAAGTTGGTGTAGAGCTCAACCT 600
Qy	682 GTACCTAACCGAATTGACTACAGTATTCGACCAACAAATCACTTCACCTGCTTTAAACAA 741
Db	601 GTACCTAACCGAATTGACTACAGTATTCGACCAACAAATCACTTCACCTGCTTTAAACAA 660
Qy	742 GCTGACTATTTCAGGCATTTACAATCTAGCTGTGGAAATATGGAATTACTTTATGACTAA 801
Db	661 GCTGACTATTTCAGGCATTTACAATCTAGCTGTGGAAATATGGAATTACTTTATGACTAA 720
Qy	802 GTTAGGTGTAGGGAACCAATCAACTCAGCTCATTAATCGGTAGCGGCTTTAATCAACGGTAA 861
Db	721 GTTAGGTGTAGGGAACCAATCAACTCAGCTCATTAATCGGTAGCGGCTTTAATCAACGGTAA 780
Qy	862 CCCTATTCTATPACGACTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACCTTCAGT 921
Db	781 CCCTATTCTATPACGACTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACCTTCAGT 840
Qy	922 CGGAACTTAATAATATGGTGCACCTACTTGGAAACCTTATCCGTAAGACCAACAG 981
Db	841 CGGAACTTAATAATATGGTGCACCTACTTGGAAACCTTATCCGTAAGACCAACAG 900
Qy	982 GGGATTTGCTCGGCACTTGTGCCAAAAGTGGTGACACAGTTCGGTTCTGTGATAGAAGA 1041

Db	901 GGGATTTGCTCGGCACTTGTCCAAAAGTGGTGACACAGGTCGGTCTCTGTGTAGTAAGA 960
Qy	1042 ACTTGACACTCATCTACTGTATAGAAACTGACTTAGATTTTATTTGTACAAAGATAGTAAC 1101
Db	961 ACTTGACACTCATCTACTGTATAGAAACTGACTTAGATTTTATTTGTACAAAGATAGTAAC 1020
Qy	1102 GTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGGCAATACATCGCGCCTGTATGTA 1161
Db	1021 GTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGGCAATACATCGCGCCTGTATGTA 1080
Qy	1162 CTCAAAAGACCGAAGGCGCACTTACTACACCATACATGACTATCAAAAGTTCAAGTCACGC 1221
Db	1081 CTCAAAAGACCGAAGGCGCACTTACTACACCATACATGACTATCAAAAGTTCAAGTCACGC 1140
Qy	1222 CAACTGCAAGATGACAAATGTAGATGTGTAAACCCCGGGTATCATATCGCAAACTA 1281
Db	1141 CAACTGCAAGATGACAAATGTAGATGTGTAAACCCCGGGTATCATATCGCAAACTA 1200
Qy	1282 TGGAGAACCGTGTCTCTAATAGATAAAACAATCATCAATGTTTTATCCTTAGCGGGAT 1341
Db	1201 TGGAGAACCGTGTCTCTAATAGATAAAACAATCATCAATGTTTTATCCTTAGCGGGAT 1260
Qy	1342 AACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAATAACAAG 1401
Db	1261 AACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAATAACAAG 1320
Qy	1402 TTCTCAAGTAATAAACAAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGTCAACAA 1461
Db	1321 TTCTCAAGTAATAAACAAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGTCAACAA 1380
Qy	1462 CTCGATCAGTAACTTTCGAATAAGTTAGAGAAAGCAACAGAAAAGTACAGCAAGTCAA 1521
Db	1381 CTCGATCAGTAACTTTCGAATAAGTTAGAGAAAGCAACAGAAAAGTACAGCAAGTCAA 1440
Qy	1522 TGTCAAACTGACTAGCACATCTGCTCTCATTTACTTATCTGTTTGTGACTATCATATCTCT 1581
Db	1441 TGTCAAACTGACTAGCACATCTGCTCTCATTTACTTATCTGTTTGTGACTATCATATCTCT 1500
Qy	1582 TGTTTTGGTATATCTTAGCCTGATTTAGCATGCTACTTAATGTACAAGAAAGGCGCA 1641
Db	1501 TGTTTTGGTATATCTTAGCCTGATTTAGCATGCTACTTAATGTACAAGAAAGGCGCA 1560
Qy	1642 ACAAAAACCTTATATGCTTGGGAATTAATCTCTAGATCAGATGAGAGCCACTACAA 1701
Db	1561 ACAAAAACCTTATATGCTTGGGAATTAATCTCTAGATCAGATGAGAGCCACTACAA 1620
Qy	1702 AATGTGAACACAGATGAGGAACGAAGTTTCCCTAAATAGTAAATTTGTGTAAGTTCTGG 1761
Db	1621 AATGTGAACACAGATGAGGAACGAAGTTTCCCTAAATAGTAAATTTGTGTAAGTTCTGG 1680
Qy	1762 TAGTCTGTGACTTACAGAGATTAAAGAAAACCTACCGGTTGTAGATGACCAAGGACGAT 1821
Db	1681 TAGTCTGTGACTTACAGAGATTAAAGAAAACCTACCGGTTGTAGATGACCAAGGACGAT 1740
Qy	1822 ATACGGGTAGAACGGTAAGAGAGCGCGCCCTCAATTTGCGAGCCAGGCTTCAACACTCC 1881
Db	1741 ATACGGGTAGAACGGTAAGAGAGCGCGCCCTCAATTTGCGAGCCAGGCTTCAACACTCC 1800
Qy	1882 GTTCTTACCGCTTCAACCGACAAACAGTCTCTCAATCATGAGCCGCGCTTAGCCAAAGTTGG 1941
Db	1801 GTTCTTACCGCTTCAACCGACAAACAGTCTCTCAATCATGAGCCGCGCTTAGCCAAAGTTGG 1860
Qy	1942 TTAGAAATGATGAAGAGAGGCAAAAATATATGGCGCTTGATATTCGGGATTCGAATC 2001
Db	1861 TTAGAAATGATGAAGAGAGGCAAAAATATATGGCGCTTGATATTCGGGATTCGAATC 1920
Qy	2002 TTATTTCTTAACAGTAGTACCTTGGCTATATCTGTAGCTCCCTTTTATATACATGGGG 2061
Db	1921 TTATTTCTTAACAGTAGTACCTTGGCTATATCTGTAGCTCCCTTTTATATAGCATGGGG 1980
Qy	2062 GCTAGCACACCTAGCGCATCTTGTAGGCATACCGACTAGGATTTCCAGGGCAGAAAGAAAG 2121

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Db 1981 GCTAGCACCTAGGATCTTTGTAGGCATACCGACTAGGATTTCCAGGGCAGAGAAAG 2040
Qy 2122 ATTACATCTACATTTGGTTCCAAATCAAGATGTAGTAGATATATAAGCAAGTGGCC 2181
Db 2041 ATTACATCTACATTTGGTTCCAAATCAAGATGTAGTAGATATATAAGCAAGTGGCC 2100
Qy 2182 CTTGAGTCTCCGTTGGCAATCTTAAATACTAGACCAACAATATAGACGAATACATCT 2241
Db 2101 CTTGAGTCTCCGTTGGCAATCTTAAATACTAGACCAACAATATAGACGAATACATCT 2160
Qy 2242 CTCTCTTATCAGATTAATGGAGCTGCMAAACACAGTGGGTGGGGGCAACCTTATCCATGAC 2301
Db 2161 CTCTCTTATCAGATTAATGGAGCTGCMAAACACAGTGGGTGGGGGCAACCTTATCCATGAC 2220
Qy 2302 CCAGATTATATAGGGGGGATAGGCAAGAACTCAATGTAGATGATGTAGTGTGCACA 2361
Db 2221 CCAGATTATATAGGGGGGATAGGCAAGAACTCAATGTAGATGATGTAGTGTGCACA 2280
Qy 2362 TCATTCTATCCCTCTGCATTTTCAAGAACATCTGAATTTTATCCGGCGCCTACTACAGGA 2421
Db 2281 TCATTCTATCCCTCTGCATTTTCAAGAACATCTGAATTTTATCCGGCGCCTACTACAGGA 2340
Qy 2422 TCAGGTTGCACCTCGAATAACCTCTATTGACATGAGTGTACCCATTACTGTACACCCAT 2481
Db 2341 TCAGGTTGCACCTCGAATAACCTCTATTGACATGAGTGTACCCATTACTGTACACCCAT 2400
Qy 2482 AATGTAATATGTCTGGATGACAGATCACTCAATTCATATCATGATTTTAGCCTTGGT 2541
Db 2401 AATGTAATATGTCTGGATGACAGATCACTCAATTCATATCATGATTTTAGCCTTGGT 2460
Qy 2542 GTGCTCCGGACATCTGCNAACAGGGAGGTATCTTTTCTACTCTGCGTTCCTCAACCTG 2601
Db 2461 GTGCTCCGGACATCTGCNAACAGGGAGGTATCTTTTCTACTCTGCGTTCCTCAACCTG 2520
Qy 2602 GACGACACCCAAATCGGAAGTCTTGAGTGTGAGTGCAACTCCCTCGGTTGTGATATG 2661
Db 2521 GACGACACCCAAATCGGAAGTCTTGAGTGTGAGTGCAACTCCCTCGGTTGTGATATG 2580
Qy 2662 CTGTGCTCGAAGTACCGGACAGAGAGAAAGATTATTAATCAGCTGTCCCTACCGGG 2721
Db 2581 CTGTGCTCGAAGTACCGGACAGAGAGAAAGATTATTAATCAGCTGTCCCTACCGGG 2640
Qy 2722 ATGTACATGGAGGTTAGGTTTCGACGGCCAGTACCACG-AAAAGNACCTAGATGTAC 2780
Db 2641 ATGTACATGGAGGTTAGGTTTCGACGGCCAGTACCACG-AAAAGNACCTAGATGTAC 2699
Qy 2781 AACATATTTCGGGACCTGGTGGCCAACTACCCAGGAGTAGGGGTGATCTTTTATTGA 2840
Db 2700 AACATATTTCGGGACCTGGTGGCCAACTACCCAGGAGTAGGGGTGATCTTTTATTGA 2759
Qy 2841 CAGCCGGGTATGGTTCTCAGTCTACGGAGGTTTAAACCCCAATTCACCCAGTGCACCTGT 2900
Db 2760 CAGCCGGGTATGGTTCTCAGTCTACGGAGGTTTAAACCCCAATTCACCCAGTGCACCTGT 2819
Qy 2901 ACAGGAAGGGAATATGTGATATACAGCGATACATGACATGCCAGATGAGCAAGA 2960
Db 2820 ACAGGAAGGGAATATGTGATATACAGCGATACATGACATGCCAGATGAGCAAGA 2879
Qy 2961 CTACAGATTTCGAATGGCCAAAGTCTTCGTATAAGCCTGGACGGTTTGGTGGAAACGCAT 3020
Db 2880 CTACAGATTTCGAATGGCCAAAGTCTTCGTATAAGCCTGGACGGTTTGGTGGAAACGCAT 2939
Qy 3021 ACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTCTTAGGCGAAGACCCGGTACTGAC 3080
Db 2940 ACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTCTTAGGCGAAGACCCGGTACTGAC 2999
Qy 3081 TGTACCGCCCAACACAGTCACTCACTGCGGGCCGAGGCGAAGATTTCTCAGATAGGGAC 3140
Db 3000 TGTACCGCCCAACACAGTCACTCACTGCGGGCCGAGGCGAAGATTTCTCAGATAGGGAC 3059
Qy 3141 ATCTCATTTCTGTATCAACGAGGTCATCATCTTCTCTCCCGGTTATTATATCTTAT 3200
Db 3060 ATCTCATTTCTGTATCAACGAGGGTCATCATCTTCTCTCCCGGTTATTATATCTTAT 3119
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Qy 3201 GACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTTATATACATTCAATGCTTCACTCG 3260
Db 3120 GACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTTATATACATTCAATGCTTCACTCG 3179
Qy 3261 GCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCAACTCGTGTGTACTGGAGT 3320
Db 3180 GCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCAACTCGTGTGTACTGGAGT 3239
Qy 3321 CTATACAGATCCATATATCCCTTAATCTTCTATAGAAACC 3358
Db 3240 CTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3277
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RESULT 6

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AA70261
ID AA70261 standard; cDNA; 3825 BP.
XX AA70261;
AC
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-APR-1991 (first entry)
XX
DE
XX
XX Sequence of Newcastle Disease Virus (NDV) F gene and HN gene.
KW Epitope; probe; diagnosis; ss.
XX
OS Newcastle disease virus.
XX
FH Key Location/Qualifiers
FT misc_feature 1..1792
FT /label= F gene
FT CDS 47..1708
FT /tag= C
FT /product= "F"
FT /note= "AAP70176"
FT misc_feature 1795..3825
FT /tag= b
FT /label= HN gene
FT CDS 1915..3648
FT /tag= d
FT /product= "HN"
FT /note= "AAP70843"
XX
XX EP227414-A.
XX
XX 01-JUL-1987.
XX
XX 16-DEC-1986; 86EP-00309804.
XX
XX 18-DEC-1985; 85GB-000311147.
XX 14-APR-1986; 86GB-00009037.
XX 15-JUL-1986; 86US-00885765.
XX
XX (NATR ) NAT RES DEV CORP.
XX
XX Bingham RW, Chambers P, Emmerson PT, Millar NS;
XX
XX WPI; 1987-179630/26.
XX P-PSDB; AAP70176, AAP70843.
XX
XX Newcastle disease virus gene clones - comprise polynucleotide(s) encoding
XX the HN and/or F protein of Newcastle disease virus RNA.
XX
XX Example; Page 11-16; 22pp; English.
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XX
XX An artificial polynucleotide encoding an HN and/or F polypeptide of
XX Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or
XX an epitopic portion of the polypeptide or an artificial nucleotide
XX complementary to the polynucleotide are claimed. The polynucleotides are
XX useful for preparing a probe for extracting similar genes from a gene
XX
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CC library or for identifying the presence of NDV virions in a sample obtd.
CC from poultry. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 27-AUG-2003 to correct OS field.)

XX
SQ Sequence 3825 BP; 1122 A; 898 C; 856 G; 949 T; 0 U; 0 Other;
Query Match 95.2%; Score 3196.4; DB 1; Length 3825;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy	1	ACGGGTAGAGATTTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	1	ACGGGTAGAGATTTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Qy	61	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGCACTGAGTTG	120
Db	61	TTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTTGCGCTGCACTGAGTTG	120
Qy	121	CATCTGTCCGGCAAACTCCATTGATGGCAGGCCTCTTGCAGCTGCGAGGAATTGGGTTAC	180
Db	121	CATCTGTCCGGCAAACTCCATTGATGGCAGGCCTCTTGCAGCTGCGAGGAATTGGGTTAC	180
Qy	181	AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Db	181	AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Qy	241	CCTCCGAATCTGCCAAGATAGGAGGATGTCGGAAGCCCTTGGATGCATACAA	300
Db	241	CCTCCGAATCTGCCAAGATAGGAGGATGTCGGAAGCCCTTGGATGCATACAA	300
Qy	301	CAGGACATTGACCACTTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAGATC	360
Db	301	CAGGACATTGACCACTTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAGATC	360
Qy	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGCTTTATAGGCGCCATTAATTGGCGGTGT	420
Db	361	TGTAACTACATCTGGAGGGGGAGACAGAAACGCTTTATAGGCGCCATTAATTGGCGGTGT	420
Qy	421	GGCTCTGGGGTTGCAACTCTCCGACCTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT	480
Db	421	GGCTCTGGGGTTGCAACTCTCCGACCTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT	480
Qy	481	ACAAATGCTGCCAACTCTCCGACCTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT	540
Db	481	ACAAATGCTGCCAACTCTCCGACCTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGT	540
Qy	541	GCATGAGGTCACGACGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	600
Db	541	GCATGAGGTCACGACGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	600
Qy	601	TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTAGACTGATCAAAATTCGACAGCA	660
Db	601	TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTAGACTGATCAAAATTCGACAGCA	660
Qy	661	AGTTGGTGTAGAGCTCAACCTGTACCTTAAAGAGAGCAATTCGAGTATTCGGACCAAAAT	720
Db	661	AGTTGGTGTAGAGCTCAACCTGTACCTTAAAGAGAGCAATTCGAGTATTCGGACCAAAAT	720
Qy	721	CACCTACCTGCTTTAAACAGCTGACTATTCAGGCACTTTTAACTAGCTGGTGAAA	780
Db	721	CACCTACCTGCTTTAAACAGCTGACTATTCAGGCACTTTTAACTAGCTGGTGAAA	780
Qy	781	TATGGATTACTTATGACTAAGTTAGGTGAGGGAACAATCAACTCAGCTCATTAATCGG	840
Db	781	TATGGATTACTTATGACTAAGTTAGGTGAGGGAACAATCAACTCAGCTCATTAATCGG	840
Qy	841	TAGCGGCTTAATCACCAGCTAACCCTATTCTATACGACTCAGAGACTCAACTCTTGGGTAT	900
Db	841	TAGCGGCTTAATCACCAGCTAACCCTATTCTATACGACTCAGAGACTCAACTCTTGGGTAT	900
Qy	901	ACAGGTAACCTACCTTTCAGTCCGGGAACCTAAATAATATATGCGTGGCACTTCTGTGAAC	960
Db	901	ACAGGTAACCTACCTTTCAGTCCGGGAACCTAAATAATATATGCGTGGCACTTCTGTGAAC	960

Qy	961	CTTATCCGTAAAGCACAAACAGGGGATTTGCCTCGCACTTGTCCCAAAAGTGGTGACACA	1020
Db	961	CTTATCTGTAAAGCACAAACAGGGGATTTGCCTCGCACTTGTCCCAAAAGTGGTGACACA	1020
Qy	1021	GGTGGTTCGTGATAGAAAGACTTCACACCTCATACTGATATAGAAACATGACATTAGATT	1080
Db	1021	GGTGGTTCGTGATAGAAAGACTTCACACCTCATATTGATATAGAAACATGACATTGGATT	1080
Qy	1081	ATATTGTACAGAAATAGTAACGTTCCCTATGTCCTGTTATTTATCTGCTTGAGCGG	1140
Db	1081	ATATTGTACAGAAATAGTAACATTCCTCTATGTCCTGTTATTTATCTGCTTGAGCGG	1140
Qy	1141	CAATACGTCGGCTGTATGTACTCAAAGACCGAAGCGCACTTACTACACCATACATGAC	1200
Db	1141	CAATACATCGGCTGTATGTACTCAAAGACCGAAGCGCACTCCTACATGCGCATATGAC	1200
Qy	1201	TATCAAAGGTTTCAGTTCATCGCCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC	1260
Db	1201	TATCAAAGGTTTCAGTTCATCGTAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCC	1260
Qy	1261	GGGTATCATATCGCAAAACATATGGAGAAGCCGTGTCTCTAATATAGATAAACAATCATGCAA	1320
Db	1261	GGGTATCATATCGCAAAACATATGGAGAAGCCGTGTCTCTAATATAGATAAACAATCATGCAA	1320
Qy	1321	TGTTTTATCTTAGCGGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACCTTATCA	1380
Db	1321	TGTTTTATCTTAGCGGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACCTTATCA	1380
Qy	1381	GAAGAAATCTCAATCAAGATTCTCAAGTAATAATAACAGGCAATCTTGTATATCTCAAC	1440
Db	1381	GAAGAAATCTCAATCAAGATTCTCAAGTAATAATAACAGGCAATCTTGTATATCTCAAC	1440
Qy	1441	TGAGCTTTGGGAATGTCACAACTCGATCAGTAATGCTTTGAATAGTTAGAGGAAAGCAA	1500
Db	1441	TGAGCTTTGGGAATGTCACAACTCGATCAGTAATGCTTTGAATAGTTAGAGGAAAGCAA	1500
Qy	1501	CAGAAACTAGACAAAGTCAATGTCACAACTGACTAGCACATCTGCTCTCATTAACCTATAT	1560
Db	1501	CAGAAACTAGACAAAGTCAATGTCACAACTGACTAGCACACATCTGCTCTCATTAACCTATAT	1560
Qy	1561	CGTTTTGACTATCATATCTCTTTGTTTGGTATATCTAGCCTGATTCTAGCATGTACCT	1620
Db	1561	CGTTTTGACTATCATATCTCTTTGTTTGGTATATCTAGCCTGATTCTAGCATGTACCT	1620
Qy	1621	AATGTACAGCAAAAGCGGCAACAAAAACCTTATTTATGGCTTGGGAATAAATCTCTAGA	1680
Db	1621	AATGTATAAGCAAAAGCGGCAACAAAAAGACCTTTATTTATGGCTTGGGAATAAATCTCTAGA	1680
Qy	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAG	1740
Db	1681	TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAG	1740
Qy	1741	TAATTTGTGTGAAAGTTCTGGTAGTCTGTGAGTTTCAAGAGATTAAAGAAAAATACCGGT	1800
Db	1741	TAATTTGTGTGAAAGTTCTGGTAGTCTGTGAGTTTCAATTCGAGAGTTTAAAGAAAAATACCGGT	1800
Qy	1801	TGTAGATGACCAAGACCATATACCGGTAGAAACCGTTAGAGAGGCGCGCCCTCAATTGC	1860
Db	1801	TGTAGATGACCAAGACCATATACCGGTAGAAACCGTTAGAGAGGCGCGCCCTCAATTGC	1860
Qy	1861	GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTACCGCAACAGTCTCAATCATGAGAC	1920
Db	1861	GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTACCGCAACAGTCTCAATCATGAGAC	1920
Qy	1921	CGCGCGTTAGCCCAAGTTGCGTTAGAGAAATGATGAAAGAGAGCAAAAAATACATGGCG	1980
Db	1921	CGCGCGTTAGCCCAAGTTGCGTTAGAGAAATGATGAAAGAGAGCAAAAAATACATGGCG	1980
Qy	1981	TTGATATTCCGGATTGCAATCTTATTTAAAGTAGTAGTACCTTGGCTATATCTGTAGCC	2040
Db	1981	TTGATATTCCGGATTGCAATCTTATTTAAAGTAGTAGTACCTTGGCTATATCTGTAGCC	2040

2041 TCCCTTTTATATAGCATGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG 2100
Db TCCCTTTTATATAGCATGGGGCTAGCACACTAGCGACCTTGTAGGCATACCGACGAG 2100
2101 ATTTCCAGGGCAGAGAAAGATTACATCTACACTTGGTTCCCAATCAAGATGTAGTAGAT 2160
Db ATTTCTAGGGCAGAGAAAGATTACATCTGCACCTTGGTTCCCAATCAAGATGTAGTAGAT 2160
2161 AGGATATATAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTGTTAAATATCTGAGACACA 2220
Db AGGATATATAAGCAAGTGGCCCTTGAAGTCTCCGTTGGCATTTGTTAAATATCTGAGACACA 2220
2221 ATTATGAACCAATAATCATCTCTCTATCAGATTAATGAGCTGCAACCAAGTGGG 2280
Db ATTATGAACCAATAATCATCTCTCTATCAGATTAATGAGCTGCGGAACAAGCGGG 2280
2281 TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAACTCATTTGTA 2340
Db TGGGGGCGACCTATCCATGACCCAGATTATATCGGGGGATAGGCAAGAACTCATTTGTA 2340
2341 GATGATGCTAGTGATGTACATCATCTTATCCCTCTGCAATTCATTTCAAGAACTCTGAAATTT 2400
Db GATGATGCTAGTGATGTACATCATCTTATCCCTCTGCAATTCATTTCAAGAACTCTGAAATTT 2400
2401 ATCCGGCGGCTACTACAGGATCAGGTGCTGCAATACCTCATTTGATGATGATGCT 2460
Db ATCCGGCGGCTACTACAGGATCAGGTGCTGCAATACCTCATTTGATGATGATGCT 2460
2461 ACCATTACTGCTACACCCCAATGTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2520
Db ACCATTACTGCTACACCCCAATGTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2520
2521 TATCAGTATTTAGCACCTTGGTGTCTCGGACATCTGCAACAGGGAGGATTTCTTTCT 2580
Db TATCAGTATTTAGCACCTTGGTGTCTCGGACATCTGCAACAGGGAGGATTTCTTTCT 2580
2581 ACTCTGGTTCATCAACCTGAGACGACACCCAAATCGGAAGTCTTGCAGTGTGAGTGCA 2640
Db ACTCTGGTTCATCAACCTGAGACGACACCCAAATCGGAAGTCTTGCAGTGTGAGTGCA 2640
2641 ACTCCCTGGTGTGATATGCTGCTCGGAAGTCTGCAAGTCTGCAAGTCTGCAAGTCTGCA 2700
Db ACTCCCTGGTGTGATATGCTGCTCGGAAGTCTGCAAGTCTGCAAGTCTGCAAGTCTGCA 2700
2701 AACTCAGTGTCTTACCGGATCGTATCGGAGGTTAGGTTGCGAGCCGACATCCAC 2760
Db AACTCAGTGTCTTACCGGATCGTATCGGAGGTTAGGTTGCGAGCCGACATCCAC 2760
2761 GAAAGACCTAGATGTACAAATTTTTCGGGACTGGGTGGCCAACTACCCAGGAGTA 2820
Db GAAAGACCTAGATGTACAAATTTTTCGGGACTGGGTGGCCAACTACCCAGGAGTA 2820
2821 GGGGGTGATTTTATGACAGCGCGGTATGTTCTCAGTCTACGAGGGTTAAACCC 2880
Db GGGGGTGATTTTATGACAGCGCGGTATGTTCTCAGTCTACGAGGGTTAAACCC 2880
2881 AATTCAACCTAGTACACTGTACAGGAGGAAATATGTATATACAGCGATACATGAC 2940
Db AATTCAACCTAGTACACTGTACAGGAGGAAATATGTATATACAGCGATACATGAC 2940
2941 ACATGCCAGATGACGAGACTACAGATTGCAATGCCAGTCTCGTATAGCCCTGGA 3000
Db ACATGCCAGATGACGAGACTACAGATTGCAATGCCAGTCTCGTATAGCCCTGGA 3000
3001 CGGTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGGTGTCAATCCTTA 3060
Db CGGTTGGTGGAAACGATACAGAGGCTATCTTATCTATCAAGGTGTCAATCCTTTG 3060
3061 GGGCAAGACCGGTACTGACTGTACCGCCCAACACAGTGCACACTCATGGGGCGGAAGGC 3120
Db GGGCAAGACCGGTACTGACTGTACCGCCCAACACAGTGCACACTCATGGGGCGGAAGGC 3120
3121 AGAATTCACAGTAGGACATCTCTTTTGTATCAACGAGGGTGCATCATCTTCTCT 3180

Db 3121 AGAATTCACAGTAGGACATCTCTTTTGTATCAGGAGGTGCATCATCTTCTCT 3180
Qy 3181 CCOCGGTTATTATATCTATGACAGTGCAGCAACAAAACAGCCACTCTTTCATAGTCTTAT 3240
Db 3181 CCOCGGTTATTATATCTATGACAGTGCAGCAACAAAACAGCCACTCTTTCATAGTCTTAT 3240
Qy 3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGGTTCAGCAAGATGCC 3300
Db 3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGGTTCAGCAAGATGCC 3300
Qy 3301 AACTCGTGTGTTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 3301 AACTCGTGTGTTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
RESULT 7
ADM78418
ID ADM78418 standard; cDNA; 5291 BP.
XX ADM78418;
XX AC
XX AC
DT 03-JUN-2004 (first entry)
XX Newcastle disease virus recombinant cDNA #14.
DE Newcastle disease virus; T7 RNA polymerase; HEP-2 cell; influenza virus;
XX infectious bursal disease virus; rotavirus; infectious bronchitis virus;
KW chicken anaemia virus; Marek's disease virus; avian Leukosis virus;
KW avian adenovirus; avian pneumovirus;
KW severe acute respiratory syndrome-causing virus; SARS;
KW human respiratory syncytial virus; human immunodeficiency virus;
KW hepatitis virus; measles virus; mumps virus; antiviral; ss.
XX
OS Newcastle disease virus.
XX
PN US2003224017-A1.
XX
XX 04-DEC-2003.
XX
XX 19-MAY-2003; 2003US-00440419.
XX
XX 05-MAY-2000; 2000WO-US006700.
PR 06-MAR-2002; 2002US-00926431.
PR 17-MAY-2002; 2002US-0381462P.
XX
XX (SAMA/) SAMAL S K.
PA (HUAN/) HUANG Z.
XX
XX Samal SK, Huang Z;
PI
XX
DR WPI; 2004-051891/05.
XX
XX Novel antigenomic RNA of Newcastle disease virus having NP, P, M, F, HN,
PT L genes and foreign nucleotide complex inserted before NP gene, between
PT P, M genes and/or between HN, L genes, useful for producing vaccine
PT vector.
XX
PS Example 3; Page 18-19; 41pp; English.
XX
CC The invention relates to an antigenomic RNA of Newcastle disease virus
CC having NP, P, M, F, HN and L genes in the 5'-3' direction, with foreign
CC nucleotide complexes inserted between genes. The invention also relates
CC to cDNA related to the RNA, a plasmid comprising the cDNA, a cell
CC comprising the RNA, cDNA or plasmid, a method of preparing the RNA and a
CC recombinant Newcastle disease virus comprising the RNA. The RNA is useful
CC for producing a recombinant Newcastle disease virus by providing cells
CC capable of synthesizing T7 RNA polymerase, transfecting the cells with a
CC plasmid comprising cDNA or a protein of interest to obtain transfected
CC cells in a medium and isolating Newcastle disease virus from a
CC supernatant of the medium, where the cells capable synthesizing T7 RNA
CC polymerase are from a cell line expressing T7 RNA polymerase or plant
CC cells, mammalian cells, avian cells or HEP-2 cells infected with a

CC vaccinia virus that can synthesise T7 RNA polymerase. The recombinant
CC virus is useful for vaccinating an avian animal against Newcastle disease
CC or an avian pathogen chosen from influenza virus, infectious bursal
CC disease virus, rotavirus, infectious bronchitis virus, chicken anaemia
CC virus, Marek's disease virus, avian Leukosis virus, avian adenovirus and
CC avian pneumovirus, where the avian animal is in need of the immunisation,
CC which involves administering the recombinant virus to the avian animal,
CC where the open reading frame of the foreign gene encodes an immunogenic
CC protein of the avian pathogen against which the avian animal is
CC immunized. The recombinant virus is also useful for immunising a mammal
CC against a non-avian pathogen such as severe acute respiratory syndrome-
CC causing virus (SARS virus), human respiratory syncytial virus, human
CC immunodeficiency virus, hepatitis virus, measles virus or mumps virus.
CC This sequence represents Newcastle disease virus recombinant cDNA of the
CC invention.
XX
SQ Sequence 5291 BP; 1565 A; 1202 C; 1186 G; 1332 T; 0 U; 6 Other;

Query Match 72.7%; Score 2441.6; DB 12; Length 5291;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 2486; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 796 GACTAAGTTAGGTGTAGGAGCAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 855
DB 1 GACTAAAGTTAGGTGTAGGAGCAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 60

QY 856 CGGTAAACCTTATCTATACAGCTCAGAGCTCAACTCACTTGGGTATACAGTAACTCTACC 915
DB 61 CGGCAACCTTATCTGTACAGCTCAGAGCTCAACTCTTGGGTATACAGTAACTCTACC 120

QY 916 TTCAGTCCGGAACCTAAATAATATGCGTGCCACCTACTTTGGAAACCTTATCCGTAAAGCAC 975
DB 121 TTCAGTCCGGAACCTAAATAATATGCGTGCCACCTACTTTGGAAACCTTATCCGTAAAGCAC 180

QY 976 AACCAGGGGATTTGCTCGCAGCTTGTCCAAAAGTGGTGACACAGCTCGGTTCTGTGAT 1035
DB 181 AACCAGGGGATTTGCTCGCAGCTTGTCCAAAAGTGGTGACACAGCTCGGTTCTGTGAT 240

QY 1036 AGAAGAACTTGACACCTCAGCTGTATAGAACTGACTTATATTTGTACAAGAAAT 1095
DB 241 AGAAGAACTTGACACCTCAGCTGTATAGAACTGACTTATATTTGTACAAGAAAT 300

QY 1096 AGTAAAGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAGCGGCAATACGTCGCGCTG 1155
DB 301 AGTAAAGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGAGCGGCAATACATCGCGCTG 360

QY 1156 TATGTACTCAAGACCGAAGCGCAGCTTACTACACATACATGACTATCAAGGTTCACT 1215
DB 361 TATGTACTCAAGACCGAAGCGCAGCTTACTACGCGCATACATGACTATCAAGGTTCACT 420

QY 1216 CATCGCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCGGGTATCATATCGCA 1275
DB 421 CATCGCTAATCGAAGATGACAACTGTAGATGTGTAAACCCCGGGTATCATATCGCA 480

QY 1276 AAACTATGGAGAACCGGTGCTCTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
DB 481 AAACTATGGAGAACCGGTGCTCTAATAGATAAACAATCATGCAATGTTTTATCCTTAGA 540

QY 1336 CGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGATCTCAAT 1395
DB 541 CGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGATCTCAAT 600

QY 1396 ACAAGATTTCTCAAGTAAATATACAGCAATCTTGATATCTCACTGAGCTTGGGAATGT 1455
DB 601 ACAAGATTTCTCAAGTAAATATACAGCAATCTTGATATCTCACTGAGCTTGGGAATGT 660

QY 1456 CAAACAACCTGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA 1515
DB 661 CAAACAACCTGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGCAAACCTAGACAA 720

QY 1516 AGTCAATGTCAAACTGACAGCAATCTGCTCTCACTTACCTATATCGTTTGTGACTATCAT 1575
DB 721 AGTCAATGTCAAACTGACAGCAATCTGCTCTCACTTACCTATATCGTTTGTGACTATCAT 780

QY 1576 ATCTCTTGTGTTTTTGGTATATCTTAGCCTGATTTCTTAGCATGCTACCTAATGTACAAGCAAA 1635
DB 781 ATCTCTTGTGTTTTTGGTATATCTTAGCCTGTTCTTAGCATGCTACCTAATGTATAAGCAAAA 840

QY 1636 GGGCAACAAAAAACCTTTATATGCGTTGGGAATAATATCTTAGATCAGATGAGAGCCAC 1695
DB 841 GGGCAACAAAAAGACCTTTATATGCGTTGGGAATAATATACCTAGATCAGATGAGAGCCAC 900

QY 1696 TACAAAAATGTGAACACACATGAGGAACGAAGTTCCTCCCTAATAGTAATTTGTGTCAAG 1755
DB 901 TACAAAAATGTGAACACACATGAGGAACGAAGTATCCNAAATAGTAATTTGTGNGAAG 960

QY 1756 TTCTGCTAGTCTGTCTAGTTTCAGAGATTAAAGAAAAAACTACCGGTTGTAGATGACCAAG 1815
DB 961 TTCTGCTAGTCTGTCTCAATTCGGAGAGTTTAGAAAAAACTACGCGTTGTAGATGACCAAG 1020

QY 1816 GACGATATACGGGTAGAACGGTAAGAGAGCGCGCCCTCAATTCGAGCCAGGCTTCACA 1875
DB 1021 GACGATATACGGGTAGAACGGTAAGAGAGCGCGCCCTCAATTCGAGCGCGGCTTCACA 1080

QY 1876 AACTCGGTTCTACCGCTTCACCGAACACAGTCTCTCAATCATGGACCGCGCGCTTAGCCAA 1935
DB 1081 AACTCGGTTCTACCGCTTCACCGACAGCAGTCTCTAGTCATGGACCGCGCGCTTAGCCAA 1140

QY 1936 GTTTCGCTTAGAAGATGATGAAAAAGAGAGGCAAAAAATACATGGCGCTTGATATTCGGGATT 1995
DB 1141 GTTTCGCTTAGAAGATGATGAAAAAGAGAGGCAAAAAATACATGGCGCTTGATATTCGGGATT 1200

QY 1996 GCAATCTTATTTCTTAACAGTAGTAGCTTGGGCTATATCTGTAGCTCCCTTTTATATAGC 2055
DB 1201 GCAATCTTACTCTTAACAGTAGTAGCTTGGGCTATATCTGTAGCTCCCTTTGTATATAGC 1260

QY 2056 ATGGGGGCTAGCACACCTAGCGATCTTGTAGCATACCGACTAGGATTTCCAGGGCAGAA 2115
DB 1261 ATGGGGGCTAGCACACCTAGCGACCTTGTAGGCATACCCAGCAAGGATTTCTAGGGCAGAA 1320

QY 2116 GAAAAGATTACATCTACACTTTGGTTCCAATCAAGATGTAGTAGAGGATATATAAGCAA 2175
DB 1321 GAAAAGATTACATCTGCACTTTGTTCCAATCAAGATGTAGTAGAGGATATATAAGCAA 1380

QY 2176 GTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTGAGACCAACAATATGAAACGAATA 2235
DB 1381 GTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAACACTGAGACCAACAATATGAAACGAATA 1440

QY 2236 ACATCTCTCTTATCAGATTAATGGAGCTGCAACAAACAGTGGGTGGGGGCGCCCTATC 2295
DB 1441 ACATCTCTCTTATCAGATTAATGGAGCTGCAACAAACAGCGGGTGGGGGCGCCCTATC 1500

QY 2296 CATGACCCAGATTTATAGGGGGATAGGCAAGAACTCATTTGTAGATGATGCTAGTGAT 2355
DB 1501 CATGACCCAGATTTATCGGGGGATAGGCAAGAACTCATTTGTAGATGATGCTAGTGAT 1560

QY 2356 GTCACATCATTTATCCCTCTGCAATTTCAAGAAACATCTGAAATTTTATCCGGGGCCCTACT 2415
DB 1561 GTCACATCATTTATCCCTCTGCAATTTCAAGAAACATCTGAAATTTTATCCGGGGCCCTACT 1620

QY 2416 ACAGGATCAGGTTGCACTCGAATACCTCATTTTGACATGAGTGTCTACCATCTACTCTAC 2475
DB 1621 ACAGGATCAGGTTGCACTCGGATACCTCATTTTGACATGAGTGTCTACCATCTACTCTAC 1680

QY 2476 ACCATAATGTAAATTTGTCTGGATGCAGAGATCACTCAATTCATATCAGTATTTAGCA 2535
DB 1681 ACTCATAAATGTAAATTTGTCTGGATGCAGAGATCACTCACTCATCATCAGTATTTAGCA 1740

QY 2536 CTTTGTGTGCTCCGGACATCTGCAACAGAGAGGATATTTCTTTTCTACTCTGCGGTTCCATC 2595
DB 1741 CTTTGTGTGCTCCGGACATCTGCAACAGAGAGGATATTTCTTTTCTACTCTGCGGTTCCATC 1800

QY 2596 AACCTGGACGACACCCAAATCGGAGTCTTCAGTGTGAGTGCAACTCCCTGGGTTGT 2655
DB 1801 AGTCTGGATGACACCCAAATCGGAAGTCTTGAGTGTGAGTGCAACTCCCTTAGGTTGT 1860

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Qy 2656 GATATGCTGTGCTCGAAAGTACCGGACACAGAGGAAGATTATTAATCACTGAGTGTCCCT 2715
Db 1861 GATATGCTGTGCTCGAAAGTACCGGACACAGAGGAAGATTATTAATCACTGAGTGTCCCT 1920
Qy 2716 ACGGGATGTACATGGAGGTAGGTTTCAGCGCCAGTACACAGAAAGAGCCTAGAT 2775
Db 1921 ACCTGATGACATGGAGGTAGGTTTCAGCGCCAGTACACAGAAAGAGCCTAGAC 1980
Qy 2776 GTCAACAATATTTCGGGACTGGGTGGCCAACTACCCAGGAGTGGGGTGGATCTTTT 2835
Db 1981 GTCAACAATATTTCGGGACTGGGTGGCCAACTACCCAGGAGTGGGGTGGATCTTTT 2040
Qy 2836 ATTGACAGCCGCTATCGTTCTAGTCTACGGAGGTAAACCCCAATTCACCCAGTAC 2895
Db 2041 ATTGACAGCCGCTATCGTTCTAGTCTACGGAGGTAAACCCCAATTCACCCAGTAC 2100
Qy 2896 ACTGTACAGGAAGGAATATGTATATACAGGATACAAATGACATGCCAGATGAG 2955
Db 2101 ACTGTACAGGAAGGAATATGTATATACAGGATACAAATGACATGCCAGATGAG 2160
Qy 2956 CAAGACTACAGATTCCGAATGGCCAACTCTTCGTATTAAGCCTGGACGGTTTGGTGGAAA 3015
Db 2161 CAAGACTACAGATTCCGAATGGCCAACTCTTCGTATTAAGCCTGGTGGTGGAAA 2220
Qy 3016 CGCATACAGAGGCTATCTTATCTATCAAGTGTCAACATCCTTAGCGGAAGACCCGGTA 3075
Db 2221 CGCATACAGAGGCTATCTTATCTATCAAGTGTCAACATCCTTTGGGCGAAGACCCAGTA 2280
Qy 3076 CTGACTGTACCGCCCAACAGTACACACTCATGGGGCCGAAGGCGAATTTCTACAGTA 3135
Db 2281 CTGACTGTACCGCCCAACAGTACACACTCATGGGGCCGAAGGCGAATTTCTACAGTA 2340
Qy 3136 GGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTCTCCCGGTTATTATAT 3195
Db 2341 GGGACATCTCATTTCTTGTATCAACGAGGCTCATCATCTCTCCCGGTTATTATAT 2400
Qy 3196 CCTATGACGTACAGCAACAAAGCCACTCTTCATAGTCTTTATATCAATTCAGCTTC 3255
Db 2401 CCTATGACGTACAGCAACAAAGCCACTCTTCATAGTCTTTATATCAATTCAGCTTC 2460
Qy 3256 ACTCGGCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCAACTCGTGTGTACT 3315
Db 2461 ACTCGGCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCAACTCGTGTGTACT 2520
Qy 3316 GGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 2521 GGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 2563
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RESULT 8

AAQ68943

ID AAQ68943 standard; DNA; 4177 BP.

XX AC AAQ68943;

XX XX

DT 25-MAR-2003 (revised)

DT 13-APR-1995 (first entry)

XX XX

DE SfiI fragment contg. Newcastle Disease Virus HN and F genes.

XX XX

KW SfiI fragment; Newcastle Disease Virus; HN gene; F gene; ss.

XX XX

OS Synthetic.

XX XX

FH Key

FT CDS

FT FT

FT FT

FT FT

FT FT

FT FT

XX XX

PN WO9419014-A1.

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01-SEP-1994.

28-FEB-1994; 94WO-US001826.

26-FEB-1993; 93US-00024156.

(SYTR) SYNTRO CORP.

(JAPG) NIPPON ZEON KK.

Cochran MD;

WPI; 1994-294007/36.

P-PSDB; AAR58858, AAR58859.

New recombinant fowl pox virus for use in vaccines - contains genes

expressing antigens of Newcastle disease virus and opt. infectious

bronchitis virus.

Disclosure; Page 63-68; 85pp; English.

Newcastle Disease Virus (NDV) HN and F genes were inserted as a SfiI

fragment into the homology vector 443-88.8 at the unique SfiI site. The

NDV HN and F genes were inserted in the same transcriptional orientation

as the ORF in the parental homology vector. The sequence of SfiI fragment

is in AAQ68943/AA58858. The inserted SfiI fragment has the

following structure: Junction A - Fragment 1 (HN, AAs 2-577) - Junction B

- Fragment 2 (F, AAs 1-553) - Junction C - Fragment 3 (pBR322) - Junction

D. Fragment 1 is approx. 1811 bp AValI to NaeI fragment of the NDV HN

cDNA clone (B1 strain). Fragment 2 is an approx 1812 bp BamHI to PetI

fragment of the full length NDV F cDNA (B1 Strain). Fragment 3 is an

approx 235 bp PetI and ScaI fragment of the plasmid pBR322. The sequences

of the Junctions are in AAQ68945, AAQ68946, AAQ68947 and AAQ68948.

(Updated on 25-MAR-2003 to correct PN field.)

Query Match

Best Local Similarity

Matches 1755; Conservative

51.9%; Score 1741.8; DB 2; Length 4177;

98.8%; Pred. No. 0;

0; Mismatches 22; Indels 0; Gaps 0;

16 TGGATCCCGGTTCCGCGCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75

2064 TCGATCCCGGTTGGCGCTCCAGGTGCGAGTGGGCTCCAGACCTTCTACCAAGAACCC 2123

76 AGCACCTATGATGCTGACTATCGGGTTGCGCTGGCACTGAGTTGCACTCTGTCGGCAAA 135

2124 AGCACCTATGATGCTGACTATCGGGTTGCGCTGGCACTGAGTTGCACTCTGTCGGCAAA 2183

136 CTCCATTGATGGCAGGCTCTTGCAGCTGCAGGAATTGTTGTTACAGGAGACAAAGCGT 195

2184 CTCCATTGATGGCAGGCTCTTGCAGCTGCAGGAATTGTTGTTACAGGAGACAAAGCGT 2243

196 CAACATATACACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCCGAATCTGCC 255

2244 CAACATATACACCTCATCCAGACAGATCAATCATAGTTAAGCTCTCCCGAATCTGCC 2303

256 CAAGGATAGGAGGATGTGCGAAAGCCCTTGGATGCATACAAAGGACATTGACAC 315

2304 AAAGGATAGGAGGATGTGCGAAAGCCCTTGGATGCATACAAAGGACATTGACAC 2363

316 TTTGCTCACCCCTTTGGTGAATCTATCCGTAGGATACAAAGTCTGTGACTACATCTGG 375

2364 TTTGCTCACCCCTTTGGTGAATCTATCCGTAGGATACAAAGTCTGTGACTACATCTGG 2423

376 AGGGGGAGACAGGGGCGCTTATAGCGCATATTGGCGGTGTGGCTCTTGGGGTGC 435

2424 AGGGGGAGACAGGGGCGCTTATAGCGCATATTGGCGGTGTGGCTCTTGGGGTGC 2483

436 AACTGCCGCAAAATAACAGCGCGCGAGCTCTGTATACAAAGCCAAATAATGCTGCCAA 495

2484 AACTGCCGCAAAATAACAGCGCGCGAGCTCTGTATACAAAGCCAAATAATGCTGCCAA 2543

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QY 556 CGGATTATCGCAACTAGCAGTGGAGTGGGGAAGATGCGAGCAGTTTGGTTAATGACCAATT 615
Db 2604 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGAGCAGTTTGGTTAATGACCAATT 2663
QY 616 TAATAAAACAGCTCAGGAATTAGACTGCAATCAATCAAAATTCACACCAAGTTGGTGTAGAGCT 675
Db 2664 TAATAAAACAGCTCAGGAATTAGACTGCAATCAATCAAAATTCACACCAAGTTGGTGTAGAGCT 2723
QY 676 CAACTGTGTACTAACCGAATTGACTACAGTATTCGGACCAACAAATCACCTTCCTGCTTT 735
Db 2724 CAACTGTGTACTAACCGAATCGACTACAGTATTCGGACCAACAAATCACCTTCCTGCTTT 2783
QY 736 AAACAAGCTGACTATTCAGGCACTTTTACAAATCTAGCTGGTGGAAATATGGATTACTTATT 795
Db 2784 AAACAAGCTGACTATTCAGGCACTTTTACAAATCTAGCTGGTGGAAATATGGATTACTTATT 2843
QY 796 GACTAAGTTAGGTAGGGAACCAATCAACTCAGCTCATTAATCGGTAGCGCTTAATCAC 855
Db 2844 GACTAAGTTAGGTATAGGGAACCAATCAACTCAGCTCATTAATCGGTAGCGCTTAATCAC 2903
QY 856 CGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTTGGGTATACAGGTAACTCTACC 915
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Db 2964 TTCAGTCGGGAACCTAAATAATATNGGTGCGCACTACTTTGGAAACCTTATCCGTAAAGCAC 3023
QY 976 AACCGGGGATTTGCTCGGCACTTGTCCCAAGTGGTGACACGTCGGTTCCTGTAT 1035
Db 3024 AACCGGGGATTTGCTCGGCACTTGTCCCAAGTGGTGACACGTCGGTTCCTGTAT 3083
QY 1036 AGAAGAACTTGACACCTCATCTGTATAGAAAATGACTTATATATTTGTACAAGAAT 1095
Db 3084 AGAAGAACTTGACACCTCATCTGTATAGAAAATGACTTATATATTTGTACAAGAAT 3143
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QY 1156 TATGTACTCAAGACCGAGCGGCACCTTACTACCAATACATCATCAATCAAGGTTTCAGT 1215
Db 3204 TATGTACTCAAGACCGAGCGGCACCTTACTACCAATATATGACTATCAAGGTCAGT 3263
QY 1216 CATCGCCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCGGGTATCATATCGCA 1275
Db 3264 CATCGCTAACTGCAAGATGACAACTGTAGATGTGTAAACCCCGGGTATCATATCGCA 3323
QY 1276 AAATAATGGAAGACCGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
Db 3324 AAATAATGGAAGACCGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 3383
QY 1336 CGGGATAACTTTAAGCTCAGTGGGNAATTCGATGTAACTTATCAGAGNAATCTCAAT 1395
Db 3384 CGGGATAACTTTAAGCTCAGTGGGNAATTCGATGTAACTTATCAGAGNAATCTCAAT 3443
QY 1396 ACAAGATTCTCAAGTAAATAACAGGCAATCTTGATATCTCAACTGAGCTGGGAATGT 1455
Db 3444 ACAAGATTCTCAAGTAAATAACAGGCAATCTTGATATCTCAACTGAGCTGGGAATGT 3503
QY 1456 CAACAACCTGATCAGTAATCCTTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA 1515
Db 3504 CAACAACCTGATCAGTAATCCTTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA 3563
QY 1516 AGTCAATGTCAAACTGACTAGCACATCTGCTCAATTACCTATATCGTTTTGACTATCAT 1575
Db 3564 AGTCAATGTCAAACTGACTAGCACATCTGCTCAATTACCTATATCGTTTTGACTATCAT 3623
QY 1576 ATCTCTTTGTTTGGTATACTTAGCCTGATTTCTAGCATGCTACCTAATGTACAAAGCAAAA 1635

Db 3624 ATCTCTTTGTTTGGTATACTTAGCCTGATTTCTAGCATGCTACCTAATGTACAAAGCAAAA 3683
QY 1636 GCGGCAACAAAAACCTTATTATGCTTGGGAATATATCTCTAGATCAGATGAGAGCCAC 1695
Db 3684 GCGGCAACAAAAAGACCTTATTATGCTTGGGAATATATCCCTAGATCAGATGAGAGCCAC 3743
QY 1696 TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAGTAATTTGTGTGAAG 1755
Db 3744 TACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAGTAATTTGTGTGAAG 3803
QY 1756 TTCTGCTAGTCTGTCTAGTTTCAGAGTTTAAAGAAAAA 1792
Db 3804 TTCTGCTAGTCTGTCTAGTTTCGAGAGTTTAAAGAAAAA 3840
RESULT 9
AAQ70570
ID AAQ70570 standard; DNA; 4177 BP.
XX AAQ70570;
AC AAQ70570;
XX 25-MAR-2003 (revised)
DT 14-APR-1995 (first entry)
XX
XX SfiI fragment contg. Newcastle disease virus HN and F genes.
XX Newcastle disease virus; HN gene; F gene; SfiI; vector 502-26.22; ss.
XX Synthetic.
FH Key Location/Qualifiers
FT CDS 115..1860
FT /*tag= a
FT /*label= AARS8598, HN
FT CDS 2095..3756
FT /*tag= b
FT /*label= AAR49141, F
XX WO9419015-A1.
XX 01-SEP-1994.
XX 28-FEB-1994; 94WO-US002252.
XX 26-FEB-1993; 93US-00024156.
XX (SYTR) SYNTRO CORP.
XX Cochran MD;
XX WPI; 1994-294008/36.
DR P-PSDB; AARS8598, AAR49141.
XX New recombinant fowl pox viruses - useful as vaccines against fowl pox virus, Newcastle Disease Virus and infectious laryngotracheitis virus.
XX Disclosure; Page 72-77; 97pp; English.
XX AAQ70570 is the SfiI fragment insert in Homology Vector 502-26.22 contg. Newcastle disease virus (NDV) HN and F genes. The structure of the fragment is: 5'- Junction A - Fragment 1 (NDV HN AAs 2-577) - Junction B - Fragment 2 (NDV P AAs 1-553) - Junction C - Fragment 3 (pBR322) - Junction D - 3'. Fragment 1 is Avail to NaeI fragment of the full length NDV HN cDNA clone (BI strain). Fragment 2 is BamHI to PstI fragment of the full length NDV F cDNA (BI strain). Fragment 3 is a PstI and ScaI fragment of pBR322. The structures of the Junctions A, B, C and D are given in AAQ70552, AAQ70553, AAQ70554 and AAQ70555 respectively. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
SQ Query Match 51.9%; Score 1741.8; DB 2; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0; Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;			
Qy	16	TGATCCCGGTTGGCGGCTCCAGGTGCAAGATGGGTCCAGACCTTCTACCAAGAACCC	75
Db	2064	TCGATCCCGGTTGGCGGCTCCAGGTGCAAGATGGGTCCAGACCTTCTACCAAGAACCC	2123
Qy	76	AGCACTATGATGCTGATATCCGGTTGGCTGGCTGCTGATGTTGATCTGTCCGGCAAA	135
Db	2124	AGCACTATGATGCTGATATCCGGTTGGCTGGCTGCTGATGTTGATCTGTCCGGCAAA	2183
Qy	136	CTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGGTTACAGGAGCAAGCGT	195
Db	2184	CTCCATTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGGTTACAGGAGCAAGCAGT	2243
Qy	196	CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCCCGAATCTGCC	255
Db	2244	CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCCCGAATCTGCC	2303
Qy	256	CAAGGATAAGAGGATGTGCGAAGCCCTTGGATGCGATACAAACAGGACATTTGACAC	315
Db	2304	AAAGGATAAGAGGATGTGCGAAGCCCTTGGATGCGATACAAACAGGACATTTGACAC	2363
Qy	316	TTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAGAGTCTGTGACTACATCTGG	375
Db	2364	TTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAGAGTCTGTGACTACATCTGG	2423
Qy	376	AGGGGGGAGACAGGGCGCCTTATAGCGCCCATTTATGGCGGTGTGGCTCTTGGGGTTGC	435
Db	2424	AGGGGGGAGACAGGGCGCCTTATAGCGCCCATTTATGGCGGTGTGGCTCTTGGGGTTGC	2483
Qy	436	AACCTCCGCAAAATAACAGCGCGCGAGCTCTGATACAGCCAAAACAAATGTCGCAA	495
Db	2484	AACCTCCGCAAAATAACAGCGCGCGAGCTCTGATACAGCCAAAACAAATGTCGCAA	2543
Qy	496	CATCCTCGGACTTAAAGAGGACATTTGGCGCAACCAATGAGGCTGTGATGAGGTCACTGA	555
Db	2544	CATCCTCGGACTTAAAGAGGACATTTGGCGCAACCAATGAGGCTGTGATGAGGTCACTGA	2603
Qy	556	CGGATATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGAGTGTGTTAATGACCAATT	615
Db	2604	CGGATATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGAGTGTGTTAATGACCAATT	2663
Qy	616	TAATAAACAGCTCAGGAATTTAGCTGATCAACAAATTTGCAAGCAAGTTGGTGTAGAGCT	675
Db	2664	TAATAAACAGCTCAGGAATTTAGCTGATCAACAAATTTGCAAGCAAGTTGGTGTAGAGCT	2723
Qy	676	CAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCAACATCACTTCACCTGCTTT	735
Db	2724	CAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCAACATCACTTCACCTGCTTT	2783
Qy	736	AAACAAGCTGACTATTTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGATTACTTTAT	795
Db	2784	AAACAAGCTGACTATTTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGATTACTTTAT	2843
Qy	796	GACTAAGTTAGGTAGGGAAACAACTCACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC	855
Db	2844	GACTAAGTTAGGTATAGGAAACAACTCACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC	2903
Qy	856	CGGTAAACCTTATCTATACGACTACAGACTCACTCTTGGGTATACAGGTAACTCTACC	915
Db	2904	CGGTAAACCTTATCTATACGACTACAGACTCACTCTTGGGTATACAGGTAACTCTACC	2963
Qy	916	TTCACTCGGGAACCTAAATAATATGCGTGGCCACCTACTTGGAAACCTTATCCGTAAGCAC	975
Db	2964	TTCACTCGGGAACCTAAATAATATGCGTGGCCACCTACTTGGAAACCTTATCCGTAAGCAC	3023
Qy	976	AACCAAGGGATTTGCCCTCGGCACCTTTGCCAAAAGTGTGACACAGGTCTGTTCTGTGAT	1035
Db	3024	AACCAAGGGATTTGCCCTCGGCACCTTTGCCAAAAGTGTGACACAGGTCTGTTCTGTGAT	3083
Qy	1036	AGAAGACTTGACACCTCACTCTGATAGAACTGACTTATGATTTATTTGTACAAGAT	1095

Db	3084	AGBAGACTTGACACCTCATCTGTATAGAACTGACTTAGATTATATTGTACAAGAT	3143
Qy	1096	AGTAACGTTCCCTATGTCCTTGGTATTTATTTCTGCTGAGGGCAATAGTCGGCTG	1155
Db	3144	AGTAACGTTCCCTATGTCCTTGGTATTTATTTCTGCTGAGGGCAATAGTCGGCTG	3203
Qy	1156	TATGTACTCAAGACCGAAGCGCCTTACTACACCATACATGACTATCAAGGTTCACT	1215
Db	3204	TATGTACTCAAGACCGAAGCGCCTTACTACACCATATATGACTATCAAGGCTCAGT	3263
Qy	1216	CATCGCCTAATGCAAGATGACCAATGATGTGTAAACCCCGGGGTATCATATCGCA	1275
Db	3264	CATCGCCTAATGCAAGATGACCAATGATGTGTGTAAACCCCGGGGTATCATATCGCA	3323
Qy	1276	AAACTATGGAAGACCGCTGTCTTAATAGATAAACAATCATGCAATGTTTATCCTTAGG	1335
Db	3324	AAACTATGGAAGACCGCTGTCTTAATAGATAAACAATCATGCAATGTTTATCCTTAGG	3383
Qy	1336	CGGGATTAACCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAGATATCTCAAT	1395
Db	3384	CGGGATTAACCTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAGATATCTCAAT	3443
Qy	1396	ACAAGATTTCTCAAGTATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	1455
Db	3444	ACAAGATTTCTCAAGTATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	3503
Qy	1456	CAACAACTCGATCAGTAATCTTTGAATAAGTTAGAGGAAGCAACAGAAACTTAGACAA	1515
Db	3504	CAACAACTCGATCAGTAATCTTTGAATAAGTTAGAGGAAGCAACAGAAACTTAGACAA	3563
Qy	1516	AGTCAATGTCAAACTGACTAGCACATCTGCTCATTTACCTATATCGTTTGTACTATCAT	1575
Db	3564	AGTCAATGTCAAACTGACTAGCACATCTGCTCATTTACCTATATCGTTTGTACTATCAT	3623
Qy	1576	ATCTCTTGTGTTTGGTATCTTACGCTGATTTAGCAATGCTACCTAATGTACAGCAAAA	1635
Db	3624	ATCTCTTGTGTTTGGTATCTTACGCTGATTTAGCAATGCTACCTAATGTACAGCAAAA	3683
Qy	1636	GGCGCAACAAAAACCTTATTATGGCTTGGGAATAATCTCTAGATCAGATGAGAGCCAC	1695
Db	3684	GGCGCAACAAAAACCTTATTATGGCTTGGGAATAATCTCTAGATCAGATGAGAGCCAC	3743
Qy	1696	TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG	1755
Db	3744	TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG	3803
Qy	1756	TTCTGTGTAGTCTGTGCTCAGAGAGTTAAGAAAAA 1792	
Db	3804	TTCTGTGTAGTCTGTGCTCAGAGAGTTAAGAAAAA 3840	

RESULT 10

AAT48510
ID AAT48510 standard; DNA; 4177 BP.

XX AAT48510;

XX 05-MAY-1997 (first entry)

XX Sfil fragment encoding Newcastle disease virus HN and F genes.

XX Fowlpox virus; FPV; recombinant virus; vector; vaccine; immunisation;
KW Newcastle disease virus; NDV; haemagglutinin; fusion protein; poultry;
ds.

XX Newcastle disease virus.

Key	Location/Qualifiers
PH CDS	115..1860
FT	/*tag= a
FT	/product= "NDV haemagglutinin"
FT	2095..3756
FT	/*tag= b

FT	/product= "NDV fusion protein"		
XX	WO9640880-A1.		
PN			
XX	19-DEC-1996.		
PD			
XX	04-JUN-1996; 96WO-US011187.		
PF			
XX	07-JUN-1995; 95US-00484790.		
PR			
XX	(SYTR) SYNTRO CORP.		
XX	Cochran MD, Junker DE, Singer PA;		
PI			
XX	WPI; 1997-087060/08.		
DR	P-PSDB; AAW10690, AAW10691.		
DR			
XX	New recombinant fowlpox virus - contg. a foreign DNA sequence inserted		
PT	into the fowlpox virus genome, used for the prodn. of vaccines.		
XX	Disclosure; Page 102-107; 134pp; English.		
PS			
XX	An SfII fragment (AA748510), contg. coding sequences for Newcastle		
CC	disease virus (NDV) haemagglutinin (HN) (AAW10690) and fusion protein (F)		
CC	(AAW10691), was inserted into homology vector 443-88.8 (see also		
CC	AA748511) at the unique SfiII site, yielding homology vector 502-26.22		
CC	(see also AA748502-05). The NDV HN and F genes were inserted in the same		
CC	transcriptional orientation as the parental homology vector. 502-26.22		
CC	was used to insert the NDV HN and F genes into fowlpox virus. The		
CC	resulting recombinant virus can be used to deliver the vaccine antigens		
CC	to poultry		
XX			
SQ	Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 51.9%; Score 1741.8; DB 2; Length 4177;			
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;			
QY	16	TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC	75
DB	2064	TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC	2123
QY	76	AGCACCTATGATGCTGACTATCCGGGTGCGCTGGCACTGAGTTGCATCTGTCCGGCAA	135
DB	2124	AGCACCTATGATGCTGACTATCCGGGTGCGCTGGCACTGAGTTGCATCTGTCCGGCAA	2183
QY	136	CTCATTTGATGGCAGGCTCTTGAGCTGCAGAAATGTGGTTACAGGAGACAAAGCGT	195
DB	2184	CTCCATTTGATGGCAGGCTCTTGAGCTGCAGAAATGTGGTTACAGGAGACAAAGCGT	2243
QY	196	CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAAGCTCTCCCGAATCTGCC	255
DB	2244	CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAAGCTCTCCCGAATCTGCC	2303
QY	256	CAAGGATAAGGAGGCATGTGCGAAAGCCCTTTGGATGCATACAACAGGACATTGACCAC	315
DB	2304	AAAGGATAAGGAGGCATGTGCGAAAGCCCTTTGGATGCATACAACAGGACATTGACCAC	2363
QY	316	TTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAAGAGTCTGTGACTACATCTGG	375
DB	2364	TTTGCTCACCCCTTGGTGACTCTATCCGTAGGATACAAGAGTCTGTGACTACATCTGG	2423
QY	376	AGGGGGAGACAGGGCGCTTATAGCGCCATTATTGGCGGTGGCTCTCGGGTTGC	435
DB	2424	AGGGGGAGACAGGGCGCTTATAGCGCCATTATTGGCGGTGGCTCTCGGGTTGC	2483
QY	436	AACTGGCGCAAAATAACAGCGCGCGAGCTCTGTATACAAGCCAAACAAAATGCTGCCAA	495
DB	2484	AACTGGCGCAAAATAACAGCGCGCGAGCTCTGTATACAAGCCAAACAAAATGCTGCCAA	2543
QY	496	CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGGTCACTGA	555
DB	2544	CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGGTCACTGA	2603
QY	556	CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTTTGTGTTAATGACCAATT	615
DB	2604	CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTTTGTGTTAATGACCAATT	2663
QY	616	TAATAAAAACAGCTCAGGAATTAGATGCAATCAAAATTCACAGCAAGTTGGTGTAGAGCT	675
DB	2664	TAATAAAAACAGCTCAGGAATTAGATGCAATCAAAATTCACAGCAAGTTGGTGTAGAGCT	2723
QY	676	CAACCTGTACCTAACCGAATTGACTACAGTATTTCGGACCAACAATCATTCACTCTGCTTT	735
DB	2724	CAACCTGTACCTAACCGAATTGACTACAGTATTTCGGACCAACAATCATTCACTCTGCTTT	2783
QY	736	AAACAAGCTGACTATTTCAGGCATTTTCAATCTAGCTGGTGGAAATATGGATTACTTATT	795
DB	2784	AAACAAGCTGACTATTTCAGGCATTTTCAATCTAGCTGGTGGAAATATGGATTACTTATT	2843
QY	796	GACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAAATCGGTAGCGGCTTAATCAC	855
DB	2844	GACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAAATCGGTAGCGGCTTAATCAC	2903
QY	856	CGGTAACCTTATTTCTATACGACTCAGACTCAACTCTTGGGTATACAGTAACTCTACC	915
DB	2904	CGGTAACCTTATTTCTATACGACTCAGACTCAACTCTTGGGTATACAGTAACTCTACC	2963
QY	916	TTCAAGTCGGGAACCTAAATAATATGCTGCACCTACTTTGGAAACCTTATCCGTAAGCAC	975
DB	2964	TTCAAGTCGGGAACCTAAATAATATGCTGCACCTACTTTGGAAACCTTATCCGTAAGCAC	3023
QY	976	AACACGGGATTTGCTCCGGCACTTGTCCAAAAGTGGTGACACAGGTCGGTTCTGTGAT	1035
DB	3024	AACACGGGATTTGCTCCGGCACTTGTCCAAAAGTGGTGACACAGGTCGGTTCTGTGAT	3083
QY	1036	AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTTAGATTATATGTTACAGAAAT	1095
DB	3084	AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTTAGATTATATGTTACAGAAAT	3143
QY	1096	AGTAAAGCTTCCCTATGTCCTTGTATTTATTTCTCTCTTGGCGGCAATACGTCGGCCTG	1155
DB	3144	AGTAAAGCTTCCCTATGTCCTTGTATTTATTTCTCTCTTGGCGGCAATACATCGCCTG	3203
QY	1156	TATGTACTCAAGACCGAAGGGCGCACTTACTACCAATCATGACTATCAAAAGGTTCAAT	1215
DB	3204	TATGTACTCAAGACCGAAGGGCGCACTTACTACCAATCATGACTATCAAAAGGTTCAAT	3263
QY	1216	CATCGCCAACTCAAGATGACACATGTAGATGTGTAAACCCCGGGTATCATATCGCA	1275
DB	3264	CATCGCTAACTGCAAGATGACACATGTAGATGTGTAAACCCCGGGTATCATATCGCA	3323
QY	1276	AAACTATGAGAAAGCCGTCTCTTAATAGATAAAACAATCATGCAATGTTTTATCTTAGG	1335
DB	3324	AAACTATGAGAAAGCCGTCTCTTAATAGATAAAACAATCATGCAATGTTTTATCTTAGG	3383
QY	1336	CGGGATAAATTAAAGGCTCAGTGGGAAATTCGATGTAATTTATCAAGAAATATCTCAAT	1395
DB	3384	CGGGATAAATTAAAGGCTCAGTGGGAAATTCGATGTAATTTATCAAGAAATATCTCAAT	3443
QY	1396	ACAAGATTCTCAAGTAATAATACAGGCAATCTTGTATATCTCAACTGAGCTTGGGAATGT	1455
DB	3444	ACAAGATTCTCAAGTAATAATACAGGCAATCTTGTATATCTCAACTGAGCTTGGGAATGT	3503
QY	1456	CAACAACCTCGATCAATTAAGTTTGAATAGGAAAGCAACAGAAAACTAGACAA	1515
DB	3504	CAACAACCTCGATCAATTAAGTTTGAATAGGAAAGCAACAGAAAACTAGACAA	3563
QY	1516	AGTCAATGTCAAACTGACTAGACATCTGCTCTCATTA CTTATATCGTTTTGACTATCAT	1575
DB	3564	AGTCAATGTCAAACTGACTAGACATCTGCTCTCATTA CTTATATCGTTTTGACTATCAT	3623
QY	1576	ATCTCTGTTTTTGGTATACCTTAGCCTGATCTTAGCATCTCACTAATGTACAGAAAA	1635
DB	3624	ATCTCTGTTTTTGGTATACCTTAGCCTGATCTTAGCATCTCACTAATGTACAGAAAA	3683

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Qy 1636 GGCGCAACAAAACCTTATTATGGCTTGGGAATATACCTAGATCAGATGAGGCCAC 1695
Dy 3684 GGCGCAACAAAAGACCTTATTATGGCTTGGGAATATACCTAGATCAGATGAGGCCAC 3743
Qy 1696 TACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAAATAGTAATTTGTGTAAG 1755
Dy 3744 TACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAAATAGTAATTTGTGTAAG 3803
Qy 1756 TTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1792
Dy 3804 TTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3840

RESULT 11
AA811147
ID AAX81147 standard; DNA; 4177 BP.
XX
AC AAX81147;
DT 07-SEP-1999 (first entry)
XX
DE Seq ID No: 12 of US9525358.
XX
KW Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;
KW Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis; ds.
XX
OS Fowlpox virus.
XX
FH Key Location/Qualifiers
FT CDS 115..1860
FT FT /*tag= a
FT FT 2095..3756
FT FT /*tag= b
XX
XX US9525358-A.
XX
XX 20-JUL-1999.
XX
XX 07-JUN-1995; 95US-00484575.
XX
XX 26-FEB-1993; 93US-00024156.
XX 28-FEB-1994; 94WO-US002252.
XX
XX (SYTR ) SYNTRO CORP.
XX
XX Junker DE, Cochran MD;
XX
XX WPI; 1999-418249/35.
XX
XX P-PSDB; AAY21982, AAY21983.
XX
XX Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys
XX against Fowlpox and Newcastle disease virus.
XX
XX Disclosure; Col 61-70; 108pp; English.
XX
XX The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX foreign DNA inserted into a region of the fowlpox virus genome
XX corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
XX host cell. The virus is used as a vaccine for immunising chickens against
XX Newcastle disease virus (NDV), Fowlpox, and Infectious Laryngotracheitis
XX
XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match 51.98; Score 1741.8; DB 2; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
Dy 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
Qy 76 AGCACTTATGATGCTGACTATCCGGGTGCGCTGGCACTGAGTGTGCAATCTGTCCGGCAA 135
Dy 76 AGCACTTATGATGCTGACTATCCGGGTGCGCTGGCACTGAGTGTGCAATCTGTCCGGCAA 135
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Dy 2124 AGCACCTATGATGCTGACTATCCGGGTGCGCTGGTACTGAGTTGCACTGTCTCGGCAAA 2183
Qy 136 CTCATTGTATGGCAGCCCTCTTGCAGCTGCAGAAATGTGGTTTACAGGAGACAAGCCGT 195
Dy 2184 CTCATTGTATGGCAGCCCTCTTGCAGCTGCAGAAATGTGGTTTACAGGAGACAAGCAGT 2243
Qy 196 CACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCTCCCGAATCTGCC 255
Dy 2244 CAAATATACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCTCCCGAATCTGCC 2303
Qy 256 CAAAGATAAGGAGGCATGTGCGAAAGCCCTTGGATGCATACAAACAGACATTTGACCAC 315
Dy 2304 AAAGGATAGGAGGCATGTGCGAAAGCCCTTGGATGCATACAAACAGACATTTGACCAC 2363
Qy 316 TTGTCTCACCCCTTGTGTGACTCTATCCGTAGGATACAAAGAGTCTGTGTGATCATCTGG 375
Dy 2364 TTGTCTCACCCCTTGTGTGACTCTATCCGTAGGATACAAAGAGTCTGTGTGATCATCTGG 2423
Qy 376 AGGGGGGAGACAGGGGGGCTTATAGCGCCATTTATGGCGTGTGGCTCTCTGGGGTTC 435
Dy 2424 AGGGGGGAGACAGGGGGGCTTATAGCGCCATTTATGGCGTGTGGCTCTCTGGGGTTC 2483
Qy 436 AACTGCGGCACAAATAACAGCGCCGAGCTCTGTATACAGCCAAACAAATCTGCGCAA 495
Dy 2484 AACTGCGGCACAAATAACAGCGCCGAGCTCTGTATACAGCCAAACAAATCTGCGCAA 2543
Qy 496 CATCTCTCCGACTTAAAGAGAGCAATTGCGCAACCAATGAGGCTGTGCATGAGTCACTGA 555
Dy 2544 CATCTCTCCGACTTAAAGAGAGCAATTGCGCAACCAATGAGGCTGTGCATGAGTCACTGA 2603
Qy 556 CGGATTTATGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTTTGTATGACCAATTT 615
Dy 2604 CGGATTTATGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTTTGTATGACCAATTT 2663
Qy 616 TAATAAAACAGCTCAGGAATTAGACTGCATCAAAATTTGACAGCAAGTTGCTGTAGAGCT 675
Dy 2664 TAATAAAACAGCTCAGGAATTAGACTGCATCAAAATTTGACAGCAAGTTGCTGTAGAGCT 2723
Qy 676 CAACTGTACTAAACCGAATTTGACTACAGTATTTGCGACCAACAAATCACTTCACTGCTTT 735
Dy 2724 CAACTGTACTAAACCGAATTTGACTACAGTATTTGCGACCAACAAATCACTTCACTGCTTT 2783
Qy 736 AAACAAGCTGACTATTTACAGCAGTTTACATCTAGCTGTGGGAATATGATTAATTTATT 795
Dy 2784 AAACAAGCTGACTATTTACAGCAGTTTACATCTAGCTGTGGGAATATGATTAATTTATT 2843
Qy 796 GACTAAGTTAGGTAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC 855
Dy 2844 GACTAAGTTAGGTATAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC 2903
Qy 856 CGGTAACCCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAACCTTACC 915
Dy 2904 CGGTAACCCCTATTCTATACGACTCAGACTCAACTCTTGGGTATACAGGTAACCTTACC 2963
Qy 916 TTCACTCGGGAACCTAAATATATGCTGTCACCTACTTGGAAACCTTATCCGTAAGCAC 975
Dy 2964 TTCACTCGGGAACCTAAATATATGCTGTCACCTACTTGGAAACCTTATCCGTAAGCAC 3023
Qy 976 AACGAGGGATTTTCCCTCGCAGCTTGTCCCAAGGTGTCACAGCTCGGTTCTGTGAT 1035
Dy 3024 AACGAGGGATTTTCCCTCGCAGCTTGTCCCAAGGTGTCACAGCTCGGTTCTGTGAT 3083
Qy 1036 AGAAGAACTTGACACCTCATCATCTGTATAGAAACCTGACTTATATTTATGTAAGAAT 1095
Dy 3084 AGAAGAACTTGACACCTCATCATCTGTATAGAAACCTGACTTATATTTATGTAAGAAT 3143
Qy 1096 AGTAAGCTTCCCTATGTCCCTCGTATTTATCTGCTTGGCGGCAATACGTCGGCTG 1155
Dy 3144 AGTAAGCTTCCCTATGTCCCTCGTATTTACTCTGCTTGGCGGCAATACATCGGCTG 3203
Qy 1156 TATGTACTCAAGACCGAGCGCACTTACTACCAATACATGACTATCAAGGTTTCAGT 1215
Dy 3204 TATGTACTCAAGACCGAGCGCACTTACTACCAATATATGACTATCAAGGCTCAGT 3263
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QY 1216 CATCGCCAACTGCAAGATGACAAATGTAGATGTATAACCCCGGGTATCATATCGCA 1275
DB |||||
DB 3264 CATCGTAACTGCAAGATGACAAATGTAGATGTATAACCCCGGGTATCATATCGCA 3323
QY 1276 AAATATGGAGAACCGGTGCTCTTAATAGATAAACAATCATGCAATGTTTATCCTTAGG 1335
DB |||||
DB 3324 AAATATGGAGAACCGGTGCTCTTAATAGATAAACAATCATGCAATGTTTATCCTTAGG 3383
QY 1336 CGGGATAACTTTAAGGCTAGTGGGAAATTCGATGTAACCTTATCAGAGNATATCTCAAT 1395
DB |||||
DB 3384 CGGGATAACTTTAAGGCTAGTGGGAAATTCGATGTAACCTTATCAGAGNATATCTCAAT 3443
QY 1396 ACAAGATCTCAAGTAAATATAACAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
DB |||||
DB 3444 ACAAGATCTCAAGTAAATATAACAGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 3503
QY 1456 CAACAACATCGATCAGTAATGCTTTGAATAGTTAGAGAAAGCAACAGAAAACTAGACAA 1515
DB |||||
DB 3504 CAACAACATCGATCAGTAATGCTTTGAATAGTTAGAGAAAGCAACAGAAAACTAGACAA 3563
QY 1516 AGTCATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATATCGTTTGTACTATCAT 1575
DB |||||
DB 3564 AGTCATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATATCGTTTGTACTATCAT 3623
QY 1576 ATCTCTTGTGTTTGGTATACTTAGCCCTGATTCTAGCATGCTACCTAATGTACAGCAAAA 1635
DB |||||
DB 3624 ATCTCTTGTGTTTGGTATACTTAGCCCTGATTCTAGCATGCTACCTAATGTACAGCAAAA 3683
QY 1636 GGCGCAACAAAAACCTTATATATGCTTGGGAATAATCTCTAGATCAGATGAGAGCCAC 1695
DB |||||
DB 3684 GGCGCAACAAAAACCTTATATATGCTTGGGAATAATACCTAGATCAGATGAGAGCCAC 3743
QY 1696 TACAAAAATGTGAACAGATGAGGACGAGGTTTCCCTAATAGTAATTTGTGTAAG 1755
DB |||||
DB 3744 TACAAAAATGTGAACAGATGAGGACGAGGTTTCCCTAATAGTAATTTGTGTAAG 3803
QY 1756 TTCTGTAGTCTCTCAGTTCAGAGAGTTAAGAAAAAA 1792
DB |||||
DB 3804 TTCTGTAGTCTCTCAGTTCAGAGAGTTAAGAAAAAA 3840
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RESULT 12

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AAZ49295
ID AAZ49295 standard; cDNA; 4177 BP.
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XX AAZ49295;
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XX 14-MAR-2000 (first entry)
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```
XX cDNA encoding NDV haemagglutinin-neuraminidase and fusion proteins.
```

```
XX Fowlpox virus; FPV; recombinant; antigenic protein; expression;
KW infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
KW Marek's disease virus; cytokeratin; promoter; homologous recombination;
KW homology vector; multivalent; live vaccine; haemagglutinin;
KW neuraminidase; fusion protein; ds.
```

```
XX Newcastle disease virus.
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```
XX Key Location/Qualifiers
```

```
XX CDS 115..1860
```

```
XX /*tag= a
```

```
XX /product= "Haemagglutinin-neuraminidase (HN, AAY58182)"
```

```
XX CDS 2095..3756
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XX /*tag= b
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```
XX /product= "Fusion (F) protein (AAY58183)"
```

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XX US6001369-A.
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```
XX 14-DEC-1999.
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```
XX 07-JUN-1995; 95US-00477459.
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XX
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PR 26-FEB-1993; 93US-00024156.
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XX 28-FEB-1994; 94WO-US002252.
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XX (SYTR ) SYNTRO CORP.
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PA Junker DE, Cochran MD;
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PI WPI; 2000-071638/06.
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```
XX P-PSDB; AAY58182, AAY58183.
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```
DR Recombinant fowlpox virus useful as a vaccine for immunizing fowl against
XX Marek's disease, Newcastle disease, Infectious laryngotracheitis Virus
XX and/or fowlpox.
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PS Claim 5; Col 61-68; 56pp; English.
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XX The invention relates to a recombinant fowlpox virus (FPV) comprising a
CC foreign DNA inserted into a 4.2 kb EcoRI fragment of the fowlpox virus
CC genome. The foreign DNA is capable of being expressed in a host cell into
CC which the fowlpox virus has been introduced and encodes an antigenic
CC protein. The antigenic protein which may be expressed includes infectious
CC laryngotracheitis virus (ILTV) glycoprotein B (gB) or glycoprotein D (gD),
CC AAY58184), Newcastle disease virus (NDV) haemagglutinin (HN, AAY58182) or
CC fusion (F) protein (AAY58183) and Marek's disease virus gB or gD. The
CC foreign DNA may alternatively encode a cytokine such as chicken
CC myelomonocytic growth factor (CMGF) or chicken interferon (cIFN). The
CC foreign DNA in the recombinant FPV is under the control of one or more
CC synthetic pox promoters, enabling control of strength and timing of
CC heterologous gene expression. The synthetic pox virus promoters that may
CC be used are based on promoters of the vaccinia virus and include early
CC promoter 1 (EPI), late promoter 1 (LPI), EPI and LP2 (AAZ49291-249294,
CC respectively). The recombinant FPV is generated via homologous
CC recombination between FPV DNA and a homology vector containing the
CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
CC the invention are used as multivalent live vaccines for immunising fowl
CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
CC present sequence represents cDNA encoding NDV haemagglutinin-
CC neuraminidase (HN) and fusion (F) proteins
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XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;
```

```
Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
```

```
Best Local Similarity 98.8%; Pred. No. 0;
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Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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```
QY 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACCTTCTACCAAGAACCC 75
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DB |||||
DB 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACCTTCTACCAAGAACCC 2123
```

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QY 76 AGCACCTATGATGCTGACTATCCGGTTCCGCTGGCAGTGGTTCATCTGTCCGGCAAA 135
```

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DB |||||
DB 2124 AGACCTATGATGCTGACTATCCGGTTCCGCTGGTACTGAGTTGATCTGTCCGGCAAA 2183
```

```
QY 136 CTCCATTGATGGCAGGCTCTTTCGAGCTGCAGGAATTGTGGTTACAGGAGACAAAGCCGT 195
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DB |||||
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```

```
QY 196 CAACATATACCTCATCTCCAGACAGGATCAATATAGTTAAAGTCTCTCCGAATCTGCC 255
```

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DB |||||
DB 2244 CAACATATACCTCATCTCCAGACAGGATCAATATAGTTAAAGTCTCTCCGAATCTGCC 2303
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QY 256 CAAGATATAGGAGGATGTGCGAAAGCCCTTGGATGCATACACAGACATTTGACAC 315
```

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DB |||||
DB 2304 AAAGGATAAGGAGGATGTGCGAAAGCCCTTGGATGCATACACAGACATTTGACAC 2363
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QY 316 TTTGTCTCACCCCTTTGGTGAATCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 375
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DB |||||
DB 2364 TTTGTCTCACCCCTTTGGTGAATCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 2423
```

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QY 376 AGGGGGAGACAGGGCGGCTTATAGGCGCCATTTATGGCGGTGGTCTTTGGGGTTGC 435
```

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DB |||||
DB 2424 AGGGGGAGACAGGGCGGCTTATATAGGCGCCATTTATGGCGGTGGTCTTTGGGGTTGC 2483
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QY 436 AACTGCCGCAAAATTAACAGCGCGCGAGCTCTGATACAAAGCCAAACAAATGCTGCCAA 495
DB 2484 AACTGCCGCAAAATTAACAGCGCGCGAGCTCTGATACAAAGCCAAACAAATGCTGCCAA 2543
QY 496 CATCCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGGTCACCTGA 555
DB 2544 CATCCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGGTCACCTGA 2603
QY 556 CGGATATTGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTTTGTATGATGCAAAATT 615
DB 2604 CGGATATTGCAACTAGCAGTGGCAGTTGGGAAGATGCAGCAGTTTGTATGATGCAAAATT 2663
QY 616 TAATAAAGAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 675
DB 2664 TAATAAAGAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 2723
QY 676 CAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCAACAAATCACTTCACCTGCTTT 735
DB 2724 CAACCTGTACTTAACCGAATTGACTACAGTATTCGGACCAACAAATCACTTCACCTGCTTT 2783
QY 736 AAACAAGCTGACTATTACAGGCACCTTTTAACTAGCTGGTGGAAATATGGATTACTTATT 795
DB 2784 AAACAAGCTGACTATTACAGGCACCTTTTAACTAGCTGGTGGAAATATGGATTACTTATT 2843
QY 796 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC 855
DB 2844 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC 2903
QY 856 CGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC 915
DB 2904 CGGTAACCCCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC 2963
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DB 2964 TTCAGTCGGGAACCTAAATAATATGCGTGGCCACCTACTTGGAAACCTTATCCGTAAGCAC 3023
QY 976 AACAGGGGATTTGCCCTCGGCACCTTGTCCCAAAAGTGGTGACACAGGTCGGTTCTGTGAT 1035
DB 3024 AACAGGGGATTTGCCCTCGGCACCTTGTCCCAAAAGTGGTGACACAGGTCGGTTCTGTGAT 3083
QY 1036 AGAAGAACTTGACACCTCATACTGATAGAACTGACTTATGATTTATGTCACAGAAAT 1095
DB 3084 AGAAGAACTTGACACCTCATACTGATAGAACTGACTTATGATTTATGTCACAGAAAT 3143
QY 1096 AGTAACGTTCCCTATGTCCTCGTGTATTTATTCCTGCTTGAGCGGCAATACGTCGGCTG 1155
DB 3144 AGTAACGTTCCCTATGTCCTCGTGTATTTATTCCTGCTTGAGCGGCAATACGTCGGCTG 3203
QY 1156 TATGTACTCAAGACCGAAGCGGCACCTTTATACACCATATATGACTATCAAAAGGCTCAGT 1215
DB 3204 TATGTACTCAAGACCGAAGCGGCACCTTTATACACCATATATGACTATCAAAAGGCTCAGT 3263
QY 1216 CATGCCAATGCAAGATGACAATGATGATGTAAACCCCGGGTATCATATCGCA 1275
DB 3264 CATGCCAATGCAAGATGACAATGATGATGTAAACCCCGGGTATCATATCGCA 3323
QY 1276 AAATATGGGAAGCCGTGTCTTAATAGATAAAACAATCATGCAATGTTTATCCTTAGG 1335
DB 3324 AAATATGGGAAGCCGTGTCTTAATAGATAAAACAATCATGCAATGTTTATCCTTAGG 3383
QY 1336 CGGATAACTTTAAGGCTCAGTGGGGAATTTCGATGTAACTTATCAGAAGAAATATCTCAAT 1395
DB 3384 CGGATAACTTTAAGGCTCAGTGGGGAATTTCGATGTAACTTATCAGAAGAAATATCTCAAT 3443
QY 1396 ACAAGATCTCAAGTAATAAACAAGCAATCTTGATATCTCACTAGCTTGGGAATGT 1455
DB 3444 ACAAGATCTCAAGTAATAAACAAGCAATCTTGATATCTCACTAGCTTGGGAATGT 3503
QY 1456 CAACAACCTCAGTATGCTTTGAAATAAGTTAGAGGAAGCAACAGAAACCTAGACAA 1515
DB 3504 CAACAACCTCAGTATGCTTTGAAATAAGTTAGAGGAAGCAACAGAAACCTAGACAA 3563

QY 1516 AGTCAATGTCAAAGTACTAGCACATCTGCTCATTTACCTATATATCGTTTGTACTATCAT 1575
DB 3564 AGTCAATGTCAAAGTACTAGCACATCTGCTCATTTACCTATATATCGTTTGTACTATCAT 3623
QY 1576 ATCTCTTTGTTTTTGGTATACTTAGCCTGATTTCTAGCATGCTTACCTAATGTACAAGCAAAA 1635
DB 3624 ATCTCTTTGTTTTTGGTATACTTAGCCTGATTTCTAGCATGCTTACCTAATGTACAAGCAAAA 3683
QY 1636 GGGCAACAAAAACCTTATTTATGGCTTGGGAATAATACCTAGATCAGATGAGAGCCAC 1695
DB 3684 GGGCAACAAAAACCTTATTTATGGCTTGGGAATAATACCTAGATCAGATGAGAGCCAC 3743
QY 1696 TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAAATAGTAATTTGTGTGAAG 1755
DB 3744 TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAAATAGTAATTTGTGTGAAG 3803
QY 1756 TTCTGGTAGTCTGTCTCAGTTCAGAGAGTAAAGAAAAA 1792
DB 3804 TTCTGGTAGTCTGTCTCAGTTCGGAGAGTTAAGAAAAA 3840

RESULT 13
AAC67862

ID AAC67862 standard; DNA; 4177 BP.

AC AAC67862;

XX 06-AUG-2003 (revised)

DT 02-MAR-2001 (first entry)

XX SfiI fragment comprising NDV HN and F genes.

XX Fowlpox virus; FPV; antiviral; antibacterial; vaccine;

KW Newcastle's disease virus; NDV; Marek's disease;

KW infectious laryngotracheitis; SfiI fragment; HN glycoprotein;

KW F glycoprotein; ds.

XX Newcastle disease virus.

XX US6136318-A.

XX 24-OCT-2000.

XX 07-JUN-1995; 95US-00486414.

XX 26-FEB-1993; 93US-00024156.

XX 28-FEB-1994; 94WO-US002252.

XX (JUNK/) JUNKER D E.

XX (COCH/) COCHRAN M D.

XX Cochran MD, Junker DE;

XX WPI; 2000-686071/67.

XX P-PSDB; AAB36038.

XX New recombinant fowlpox virus useful as vaccines contains foreign DNA inserted into specific non-essential region of the genome.

XX Disclosure; Col 59-68; 56pp; English.

XX The present sequence is provided in a specification relating to a recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA can be expressed in host cells infected with FPV. The recombinant FPV may be used in vaccines to protect animals (especially chickens) against fowlpox and, depending on the source of the foreign DNA, other diseases, particularly Newcastle's disease, Marek's disease or infectious laryngotracheitis. (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 4177 BP; 1199 A; 980 C; 910 G; 1088 T; 0 U; 0 Other;

Query Match

51.9%; Score 1741.8; DB 3; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0; Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;									
QY	16	TGGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC	75						
Db	2064	TCGATCCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC	2123						
QY	76	AGCACCTATGATGCTGACTATCCGGGTGGCGCTGGCACTGAGTTGCATCTGTCCGGCAAA	135						
Db	2124	AGCACCTATGATGCTGACTATCCGGGTGGCGCTGGCACTGAGTTGCATCTGTCCGGCAAA	2183						
QY	136	CTCCATTTGATGGCAGGCTCTTGAGCTGCAGGAAATTTGGTTTACAGGAGACAAAGCCGT	195						
Db	2184	CTCCATTTGATGGCAGGCTCTTGAGCTGCAGGAAATTTGGTTTACAGGAGACAAAGCAGT	2243						
QY	196	CCACATATACACCTCATCCAGACAGATCAATCATAGTTAAAGCTCTCCCGAATCTGCC	255						
Db	2244	CAACATATACACCTCATCCAGACAGATCAATCATAGTTAAAGCTCTCTCCGAAATCTGCC	2303						
QY	256	CAAGGATAAGAGGCGATGTGCGAAAGCCCTTTGGATGCATACAAACAGGACATTTGACCAC	315						
Db	2304	AAAGGATAAGAGGCGATGTGCGAAAGCCCTTTGGATGCATACAAACAGGACATTTGACCAC	2363						
QY	316	TTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAAGAGTCTGTGTACTCATCTGG	375						
Db	2364	TTTGCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAAGAGTCTGTGTACTCATCTGG	2423						
QY	376	AGGGGGAGACAGGGGGCTTATAGCGCCATTTATGGCGGTGTGGCTCTGGGGTTGC	435						
Db	2424	AGGGGGAGACAGGGGGCTTATAGCGCCATTTATGGCGGTGTGGCTCTTTGGGGTTGC	2483						
QY	436	AACTGCGCGCAAAATAACAGCGCGCGAGCTCTGTATACAGCCAAACAAATCGTCCCAA	495						
Db	2484	AACTGCGCGCAAAATAACAGCGCGCGAGCTCTGTATACAGCCAAACAAATGCTGCCAA	2543						
QY	496	CATCCTCCGATTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGTGCATGAGGTCTACTGA	555						
Db	2544	CATCCTCCGATTTAAAGAGAGCAATTCGCGCAACCAATGAGGCTGTGCATGAGGTCTACTGA	2603						
QY	556	CGGATTTACCACTAGCAGTGGCAGTTGGGAGATGCAGCAGTTTGTAAATGACCAATTT	615						
Db	2604	CGGATTTACCACTAGCAGTGGCAGTTGGGAGATGCAGCAGTTTGTAAATGACCAATTT	2663						
QY	616	TAATAAAACAGCTCAGGAATTTAGACTGTCATCAAAATTTGCACGCAAGTTGGTGTAGAGCT	675						
Db	2664	TAATAAAACAGCTCAGGAATTTAGACTGTCATCAAAATTTGCACGCAAGTTGGTGTAGAGCT	2723						
QY	676	CAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCAAAATCACTTCACCTGCTTT	735						
Db	2724	CAACCTGTACCTAACCGAATTTGACTACAGTATTCGGACCAAAATCACTTCACCTGCTTT	2783						
QY	736	AAACAAGCTGACTATTTACGACCTTTTACAACTAGCTGGTGGAAATATGGATTACTTATTT	795						
Db	2784	AAACAAGCTGACTATTTACGACCTTTTACAACTAGCTGGTGGAAATATGGATTACTTATTT	2843						
QY	796	GACTTAAGTTAGGTGATGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC	855						
Db	2844	GACTTAAGTTAGGTGATGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGCTTAATCAC	2903						
QY	856	CGGTAACCCCTATTTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC	915						
Db	2904	CGGTAACCCCTATTTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTTACC	2963						
QY	916	TTCAAGTCGGGAACCTAAATAATATGCGTGCACCTACTTGGAAACCTTATCCGTAAAGCAC	975						
Db	2964	TTCAAGTCGGGAACCTAAATAATATGCGTGCACCTACTTGGAAACCTTATCCGTAAAGCAC	3023						
QY	976	AACACAGGGATTTGGCTCGGCACCTTTGCCAAAGTGGTGACACAGTGGTTCTGTGAT	1035						
Db	3024	AACACAGGGATTTGGCTCGGCACCTTTGCCAAAGTGGTGACACAGTGGTTCTGTGAT	3083						
QY	1036	AGAAGAACTTGACACCTCTACTGTATAGAAACTGACTTAGATTTTATATTTGTACAAGAAT	1095						
Db									

3084	AGAAGAACTTGACACCTCTACTGTATAGAAACTGACTTAGATTTTATATTTGTACAAGAAT	3143
1096	AGTAAACGTTCCCTCTATCTCCCTGGTATTTTATCTCTCTTTGAGCGGCAATACGTCGCGCTG	1155
3144	AGTAAACGTTCCCTCTATCTCTCCCTGGTATTTTATCTCTCTTTGAGCGGCAATACATCGCGCTG	3203
1156	TATGTACTCAAAAGACCGAAGGCGCACTTACTACACCATATGACTATCAAAAGGTTCACT	1215
3204	TATGTACTCAAAAGACCGAAGGCGCACTTACTACACCATATGACTATCAAAAGGTTCACT	3263
1216	CATCGGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCGGGTATCATATCGCA	1275
3264	CATCGGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCGGGTATCATATCGCA	3323
1276	AAACTATGAGAGCGCTGTCTCTAATAGATAAAACATCATGCAATGTGTTTATCTCTTAGG	1335
3324	AAACTATGAGAGCGCTGTCTCTAATAGATAAAACATCATGCAATGTGTTTATCTCTTAGG	3383
1336	CGGGATAACTTTAAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAAGAATATCTCAAT	1395
3384	CGGGATAACTTTAAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAAGAATATCTCAAT	3443
1396	ACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	1455
3444	ACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT	3503
1456	CAACAACTCGATCAAGTAAATGCTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA	1515
3504	CAACAACTCGATCAAGTAAATGCTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA	3563
1516	AGTCAATGTCAAACTGACTAGCACATCTCTCTCAATTACCTATATCGTTTGTGACTATCAT	1575
3564	AGTCAATGTCAAACTGACTAGCACATCTCTCTCAATTACCTATATCGTTTGTGACTATCAT	3623
1576	ATCTCTGTTTGTGGTATACCTTACCTGATTTAGCATGCTACCTTAATGTACAGAAAA	1635
3624	ATCTCTGTTTGTGGTATACCTTACCTGATTTAGCATGCTACCTTAATGTACAGAAAA	3683
1636	GGCGCAACAAAAACCTTATATGCTTGGGAATATATCTAGATCAGATGAGAGCCAC	1695
3684	GGCGCAACAAAAACCTTATATGCTTGGGAATATATCCCTAGATCAGATGAGAGCCAC	3743
1696	TACAAAAATGTGAACACACAGATGAGGAACGAAGGTTTCCCTAATAGTAAATTTGTGTGAAG	1755
3744	TACAAAAATGTGAACACACAGATGAGGAACGAAGGTTTCCCTAATAGTAAATTTGTGTGAAG	3803
1756	TTCTGTGATGCTGTCTAGTTTCAGAGATTAAAGAAAAA	1792
3804	TTCTGTGATGCTGTCTAGTTTCAGAGATTAAAGAAAAA	3840

RESULT 14
ABK90556
ID ABK90556 standard; cDNA; 3570 BP.
XX
AC ABK90556;
XX
DT 15-NOV-2002 (first entry)
XX
Newcastle disease virus (NDV) fusion gene.
DE
XX
XX Newcastle disease virus; gene; ss; novel recombinant avian herpesvirus;
KW NAHV, herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;
KW infectious laryngotracheitis; virucide; immunostimulant; vaccine; NDV.
XX
OS Newcastle disease virus.
XX
XX
FH Key Location/Qualifiers
FT CDS 1194..2888
FT /tag= a
FT /product= "Newcastle disease virus protein"
FT /transl_except= (pos:1353..1355, aa:Xaa)
FT /note= "Xaa= unknown"

XX US2002081316-A1.
XX 27-JUN-2002.
XX 14-JUN-2001; 2001US-00881457.
XX 12-JUN-1992; 92US-00898087.
XX 26-FEB-1993; 93US-00023610.
XX 14-JUN-1993; 93WO-US005681.
XX 09-AUG-1994; 94US-00288065.
XX 09-AUG-1995; 95WO-US010245.
XX 13-JUN-1996; 96US-00663566.
XX 21-FEB-1997; 97US-00804372.
XX 25-OCT-1999; 99US-00426352.
XX (COCH/) COCHRAN M D.
XX (COOK/) COOK S M.
XX (WILD/) WILD M A.
XX Cochran MD, Cook SM, Wild MA;
XX WPI; 2002-635456/68.
XX P-PSDB; ABG31709.
XX Novel recombinant avian herpesvirus comprising unique long and repeat
XX viral genome regions of herpes virus of turkeys, unique short viral
XX genome region of Marek's disease virus, and optional foreign DNA
XX sequence.
XX Disclosure; Page 12-14; 26pp; English.
XX The invention relates to a novel recombinant avian herpesvirus (NAHV)
XX comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat
XX viral genome region and a Marek's disease virus unique short (US) viral
XX genome region where at least one foreign DNA sequence is inserted within
XX a US2 gene of the US region of the NAHV, and is capable of being
XX expressed in a host cell. NAHV is useful for producing vaccines used for
XX immunising an avian species against Newcastle disease, infectious
XX laryngotracheitis and Marek's disease. This sequence represents a
XX Newcastle disease virus (NDV) fusion gene
XX
XX Sequence 3570 BP; 982 A; 857 C; 845 G; 885 T; 0 U; 1 Other;
XX
XX Query Match 50.7%; Score 1701.6; DB 6; Length 3570;
XX Best Local Similarity 98.4%; Pred. No. 0;
XX Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;
XX
XX 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
XX 1199 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 1258
XX
XX 76 AGCACTATGATGCTGACTATCCGGGTTGGCTGGCACTGAGTTGCATCTGTCCGGCAAA 135
XX 1259 AGCACTATGATGCTGACTATCCGGGTTGGCTGGCACTGAGTTGCATCTGTCCGGCAAA 1318
XX
XX 136 CTCATTGATGGCAGGCTTTTCAGCTGCAAGAAATTTGTTTACAGGAGACAAAGCCGT 195
XX 1319 CTCATTGATGGCAGGCTTTTCAGCTGCAAG-ACTNTGTTACAGGAGACAAAGCAAT 1377
XX
XX 196 CAACATATACCTTCATCCAGACAGGATCAATCATAGTTAAGTCTCTCCGATCTGCC 255
XX 1378 CAACATATACCTTCATCCAGACAGG-TCAATCATAT-TTAAGCTCTCCGATCTGCC 1435
XX
XX 256 CAAGGATAAGGAGCATGTGCAAGCCCTTGGATGCATACAAAGGACATTTGACCAC 315
XX 1436 AAGGATTAAGGAGCATGTGCAAGCCCTTGGATGCATACAAAGGACATTTGACCAC 1495
XX
XX 316 TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAAAGAGTCTGTGATCATCTGG 375
XX 1496 TTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAAAGAGTCTGTGATCATCTGG 1555
XX
XX 376 AGGGGGAGACAGGGGGCCCTTATAGCGCCATTAATTTGGCGGTGTGGCTCTTGGGGTTGC 435

Db 1556 AGGGGGAGACAGGGGGCCCTTATAGCGCCATTAATTTGGCGGTGTGGCTCTTGGGGTTGC 1615
Qy 436 AACTGCCGCAAAATAAACAGCGCGCAGCTCTGTATACAAAGCCAAAACAAATGTGCGCAA 495
Db 1616 AACTGCCGCAAAATAAACAGCGCGCAGCTCTGTATACAAAGCCAAAACAAATGTGCGCAA 1675
Qy 496 CATCCTCCGACTTAAAGAGAGCATTTGCGGCAACCAATGAGGCTGTGCATGAGGTCACTGA 555
Db 1676 CATCCTCCGACTTAAAGAGAGCATTTGCGGCAACCAATGAGGCTGTGCATGAGGTCACTGA 1735
Qy 556 CGGATTAATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGCAGTTGTTAATGACCAAT 615
Db 1736 CGGATTAATCGCAACTAGCAGTGGCAGTTGGGAAGATGCGCAGTTGTTAATGACCAAT 1795
Qy 616 TAATAAAACAGCTCAGGAATTTAGATCGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 675
Db 1796 TAATAAAACAGCTCAGGAATTTAGATCGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 1855
Qy 676 CAACCTGTACTTAACCGAATTTGACTACAGTATTCGGACCAAAATCACTTCCACTGCTTT 735
Db 1856 CAACCTGTACTTAACCGAATTTGACTACAGTATTCGGACCAAAATCACTTCCACTGCTTT 1915
Qy 736 AAACAAGCTGACTTATTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGAATTAATTT 795
Db 1916 AAACAAGCTGACTTATTCAGGCACCTTTACAATCTAGCTGGTGGAAATATGGAATTAATTT 1975
Qy 796 GACTAAGTTAGGTGTAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 855
Db 1976 GACTAAGTTAGGTGTAGGGAACCAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 2035
Qy 856 CGGTAAACCTTATCTATACGACTCAGACACTCAACTCTTGGGTATACAGGTAACTCTACC 915
Db 2036 CGGTAAACCTTATCTATACGACTCAGACACTCAACTCTTGGGTATACAGGTAACTCTACC 2095
Qy 916 TTCAGTCGGGAACCTTAATTAATGCGTGCACCTACTTGGAAACCTTATCCGTAAGCAC 975
Db 2096 TTCAGTCGGGAACCTTAATTAATGCGTGCACCTACTTGGAAACCTTATCCGTAAGCAC 2155
Qy 976 AACCCAGGGGATTTGCCCTCGGCACCTTGTCCAAAGTGGTGACACAGGTTCGGTCTGTGAT 1035
Db 2156 AACCCAGGGGATTTGCCCTCGGCACCTTGTCCAAAGTGGTGACACAGGTTCGGTCTGTGAT 2215
Qy 1036 AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTATAGATTTATTTGTACAAAGAT 1095
Db 2216 AGAAGAACTTGACACCTCATCTGTATAGAACTGACTTATAGATTTATTTGTACAAAGAT 2275
Qy 1096 AGTAAAGTTCCCTATGTCCCTCGTATTTATTTCTGCTTTCAGCGGCAATACGTCGGCTG 1155
Db 2276 AGTAAAGTTCCCTATGTCCCTCGTATTTACTCTGCTTGGCGGCAATACATCGGCTG 2335
Qy 1156 TATGTACTCAAAGACCGAGCGCCTTACTACACCATATGACTTATCAAAGGTTTCAGT 1215
Db 2336 TATGTACTCAAAGACCGAGCGCCTTACTACACCATATGACTTATCAAAGGTTTCAGT 2395
Qy 1216 CATCGCCAACTGCAAGATGACAACTGATGTGTAAACCCCGGGGTATCATATCGCA 1275
Db 2396 CATCGCTAACTGCAAGATGACAACTGATGTGTAAACCCCGGGGTATCATATCGCA 2455
Qy 1276 ARACTATGGAGAGCGGTCTCTTAATAGATAAACCAATCATGCAATGTTTTATCCTTAGG 1335
Db 2456 ARACTATGGAGAGCGGTCTCTTAATAGATAAACCAATCATGCAATGTTTTATCCTTAGG 2515
Qy 1336 CGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGTAATTTATCAGAAGAAATATCTCAAT 1395
Db 2516 CGGGATAAATTTAAGGCTCAGTGGGGAATTCGATGTAATTTATCAGAAGAAATATCTCAAT 2575
Qy 1396 ACAAGATTTCAAGTAAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
Db 2576 ACAAGATTTCAAGTAAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 2635
Qy 1456 CAACAATCGATCAGTAATGCTTTGATAGATTTAGGGAAGCAACAGAAATCTAGACAA 1515

Db 2636 CAACAACCTCGATCAGTAATGCTTGAATAAGTTAGAGAAAGCAACAGAAAACTAGACAA 2695
QY 1516 AGTCAATGTCARACTGACTAGCACATCTGCTCATTTACTATATGTTTGGACTATCAT 1575
Db 2696 AGTCAATGTCARACTGACTAGCACATCTGCTCATTTACTATATGTTTGGACTATCAT 2755
QY 1576 ATCTCTGTTGTTTGGTATACCTTAGCCCTGATTCTTAGCATGCTACCTTAATGTACAAGCAAAA 1635
Db 2756 ATCTCTGTTGTTGTTATACCTTAGCCCTGATTCTTAGCATGCTACCTTAATGTACAAGCAAAA 2815
QY 1636 GGGCCAAACAAAACCTTATATGCTTGGGAATAATATCTTAGATCAAGAGAGCCAC 1695
Db 2816 GGGCCAAACAAAAGACCTTATATGCTTGGGAATAATATCTTAGATCAAGAGAGCCAC 2875
QY 1696 TACAAAATCTGAACACAGATGAGGACGAAGCTTTCCCTAATAGTAATTTGTGTGAAG 1755
Db 2876 TACAAAATCTGAACACAGATGAGGACGAAGCTTTCCCTAATAGTAATTTGTGTGAAG 1935
QY 1756 TTCTGCTAGTCTGCTCAGTTTCAGAGAGTTAAGAAAAAA 1792
Db 2936 TTCTGCTAGTCTGCTCAGTTTCGGAGAGTTAAGAAAAAA 2972

RESULT 15
AAT18203
ID AAT18203 standard; DNA; 1662 BP.
AC AAT18203;
DT 04-MAR-1997 (first entry)
XX Newcastle disease virus F gene.
XX Turkey herpes virus; recombinant virus; vaccine; prophylaxis;
KW immunisation; avian virus; infectious bronchitis virus;
KW infectious bursal disease virus; Newcastle disease virus;
KW Marek's disease virus; infectious laryngotracheitis virus; IBV; IBDV;
KW NDV; MDV; ILV; ds.
XX Newcastle disease virus.
XX
FH Key Location/Qualifiers
FT 1. .1662
FT CDS /tag= a
FT /product= "NDV F gene product"
XX
PN W09605291-A1.
XX
XX 22-FEB-1996.
XX
XX 09-AUG-1995; 95WO-US010245.
XX
XX 09-AUG-1994; 94US-00288065.
PR 22-DEC-1994; 94US-00362240.
XX
XX (SYTR) SYNTRO CORP.
XX
PI Cochran MD, Junker DE, Wild MA, Singer PA;
XX
XX WPI; 1996-139689/14.
DR P-PSDB; AAW06828.
XX
XX Recombinant turkey herpes viruses contg. foreign DNA encoding a cytokine
PT - useful in vaccines to protect against Marek's disease virus and other
PT avian viruses.
XX
PS Disclosure; Page 177-179; 249pp; English.
XX
XX Recombinant turkey herpes virus (rTH) which comprise a foreign DNA
CC sequence encoding a cytokine inserted into a XhoI site within an EcoRI #9
CC genomic fragment, where the cytokine can be expressed in host cells
CC infected with the virus can be used in vaccines to protect turkeys
XX against avian viruses. The recombinant viruses can be used for immunising

CC birds against infectious bronchitis virus (IBV), infectious bursal
CC disease virus (IBDV), Marek's disease virus (MDV) infectious
CC laryngotracheitis virus (ILV) and Newcastle disease virus (NDV). They may
CC also be used in multivalent vaccines to protect against two or more of
CC these avian viruses. This sequence is the F gene of the Newcastle disease
CC virus and encodes an antigen which can be used in the recombinant
CC vaccines
XX
SQ Sequence 1662 BP; 507 A; 390 C; 353 G; 412 T; 0 U; 0 Other;
Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 47 ATGGGCTCCAGACCTTTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGGTTCGG 106
Db 1 ATGGGCTCCAGACCTTTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGGTTCGG 60
QY 107 CTGGCACTGAGTTGATCTGTCCGGCAAACTCCATTGATGGCAGGCTCTTGCACTGCA 166
Db 61 CTGGTACTGAGTTGATCTGTCCGGCAAACTCCATTGATGGCAGGCTCTTGCACTGCA 120
QY 167 GGAATTTGGTTACAGGAGACAAGCCGTCACATATACACCTCATCCAGACAGATCA 226
Db 121 GGAATTTGGTTACAGGAGACAAGCCAGTCACATATACACCTCATCCAGACAGATCA 180
QY 227 ATCATAGTTAAGCTCTCTCCGAATCTGCCAAGGATAGGAGGCATGTGCGAAAGCCCC 286
Db 181 ATCATAGTTAAGCTCTCTCCGAATCTGCCAAGGATAGGAGGCATGTGCGAAAGCCCC 240
QY 287 TTGGATGCATACAACAGGACATTTGACCACTTTGCTCACCCCCCTTGGTGACTCTATCCGT 346
Db 241 TTGGATGCATACAACAGGACATTTGACCACTTTGCTCACCCCCCTTGGTGACTCTATCCGT 300
QY 347 AGATAACAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCTTATAGCGGCC 406
Db 301 AGGATAACAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCTTATAGCGGCC 360
QY 407 ATTATTGGCGGTGTGCTCTTGGGGTTGCAACTGCGGCACAAATAACACGGCGCGCAGCT 466
Db 361 ATTATTGGCGGTGTGCTCTTGGGGTTGCAACTGCGGCACAAATAACACGGCGCGCAGCT 420
QY 467 CTGATAACAAGCCAAACAAATGCTGCCAACATCTCTCCGACTTAAAGAGAGCAATTGCCGA 526
Db 421 CTGATAACAAGCCAAACAAATGCTGCCAACATCTCTCCGACTTAAAGAGAGCAATTGCCGA 480
QY 527 ACCAATGAGGCTGTGCATGAGTCACTGACGATATCCGAACCTAGCAGTGGCAGTTGG 586
Db 481 ACCAATGAGGCTGTGCATGAGTCACTGACGATATATCGCAACTAGCAGTGGCAGTTGG 540
QY 587 AAGATGCAGCAGTTTGTAAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATC 646
Db 541 AAGATGCAGCAGTTTGTAAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATC 600
QY 647 AAAATTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTA 706
Db 601 AAAATTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTA 660
QY 707 TTCGGACCAAAATCACTTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTTCAAT 766
Db 661 TTCGGACCAAAATCACTTCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTTCAAT 720
QY 767 CTAGCTGGTGGAAATATGATTACTTATTGACTTAAGTTAGGTGTAGGGAAACCAATCAATC 826
Db 721 CTAGCTGGTGGAAATATGATTACTTATTGACTTAAGTTAGGTGTAGGGAAACCAATCAATC 780
QY 827 AGCTCAATTAATCGGTAGCGGCTTAATCACCGGTAAACCTTATTCTATACGACTCACAGACT 886
Db 781 AGCTCAATTAATCGGTAGCGGCTTAATCACCGGTAAACCTTATTCTATACGACTCACAGACT 840
QY 887 CAACTCTTGGGTATACAGGTAATCTTACCTTCAGTGGGAAACCTAATAATATATCGTGCC 946
Db 841 CAACTCTTGGGTATACAGGTAATCTTACCTTCAGTGGGAAACCTAATAATATATCGTGCC 900

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QY	361	TGTGACTACATCTGGAGGGGGAGACAGGGGCGCCTTATAGGCGCCATTTATGGCGGTGT	420
Db	4858	TGTGACTACATCTGGAGGGGGAGACAGGGGCGCCTTATAGGCGCCATTTATGGCGGTGT	4917
QY	421	GGCTCTTGGGGTTCGAACTGCGCGCAAAATAACAGCGGCGCGAGCTCTGATACAAAGCAA	480
Db	4918	GGCTCTTGGGGTTCGAACTGCGCGCAAAATAACAGCGGCGCGAGCTCTGATACAAAGCAA	4977
QY	481	ACAAATGCTGCCAATCTCCGACTTAAGAGAGCATTTGCCGACCAATCAGGCTGT	540
Db	4978	ACAAATGCTGCCAATCTCCGACTTAAGAGAGCATTTGCCGACCAATCAGGCTGT	5037
QY	541	GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	600
Db	5038	GCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	5097
QY	601	TGTTAATGACCAATTTAATAAACAAGCTCAGGAATAGACTGCATGCAAAATTCGACGCA	660
Db	5098	TGTTAATGACCAATTTAATAAACAAGCTCAGGAATAGACTGCATGCAAAATTCGACGCA	5157
QY	661	AGTTGGTGTAGACTCAACCTGTACCTTAACCGAATTCAGCTACAGTATTCGGACCAAAAT	720
Db	5158	AGTTGGTGTAGACTCAACCTGTACCTTAACCGAATTCAGCTACAGTATTCGGACCAAAAT	5917
QY	721	CACCTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTTACAATCTAGCTGGTGAAA	780
Db	5218	CACCTTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTTACAATCTAGCTGGTGAAA	5277
QY	781	TATGGATTACTTATGCTAAGTTAGGTGAGGAAACAATCAACTCAGCTCATTAATTCGG	840
Db	5278	TATGGATTACTTATGCTAAGTTAGGTGAGGAAACAATCAACTCAGCTCATTAATTCGG	5337
QY	841	TAGGGCTTAATCACGGTTAACCTTATCTATAGGACTCACAGACTCAACTCTTGGGTAT	900
Db	5338	TAGGGCTTAATCACGGTTAACCTTATCTATAGGACTCACAGACTCAACTCTTGGGTAT	5397
QY	901	ACAGGTTAACTCTACCTTCAGTCGGGAACCTTAAATATATCGCTGCCACCTTACTTGGAAAC	960
Db	5398	ACAGGTTAACTCTACCTTCAGTCGGGAACCTTAAATATATCGCTGCCACCTTACTTGGAAAC	5457
QY	961	CTTATCCGTAAAGCAACACAGGGGATTTGCCTCGGCACTTTGTCCCAAAAGTGTGACACA	1020
Db	5458	CTTATCCGTAAAGCAACACAGGGGATTTGCCTCGGCACTTTGTCCCAAAAGTGTGACACA	5517
QY	1021	GGTCGGTCTGTGATGAGAACTTGTGACACTCATACTGTATAGAAACTGACTTAGATTT	1080
Db	5518	GGTCGGTCTGTGATGAGAACTTGTGACACTCATACTGTATAGAAACTGACTTAGATTT	5577
QY	1081	ATATTGTACAAGAAATAGTAACTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	1140
Db	5578	ATATTGTACAAGAAATAGTAACTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	5637
QY	1141	CAATACGTCCGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACCATACATGAC	1200
Db	5638	CAATACGTCCGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACCATACATGAC	5697
QY	1201	TATCAAAAGGTTCACTCATCCCAACTGCAAGATGACAAATGTAGATGTGTAAACCCCCC	1260
Db	5698	TATCAAAAGGTTCACTCATCCCAACTGCAAGATGACAAATGTAGATGTGTAAACCCCCC	5757
QY	1261	GGGTATCATATCGCAAACTTATCGAGAAGCCGTGCTCTTAATAGATAAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAACTTATCGAGAAGCCGTGCTCTTAATAGATAAAACAATCATGCAA	5817
QY	1321	TGTTTTATTCCTTAGCGGGGATACTTTTAAGGCTCAGTGGGGAATTCGATGAACCTTATCA	1380
Db	5818	TGTTTTATTCCTTAGCGGGGATACTTTTAAGGCTCAGTGGGGAATTCGATGAACCTTATCA	5877
QY	1381	GAAGAATATCTCAATACAAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
Db	5878	GAAGAATATCTCAATACAAAGATTTCTCAAGTAATAATAACAGGCAATCTTTGATATCTCAAC	5937

QY	1441	TGAGCTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTGAAATAAGTTAGAGGAAGCAA	1500
Db	5938	TGAGCTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTGAAATAAGTTAGAGGAAGCAA	5997
QY	1501	CAGAAACTAGACAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATAT	1560
Db	5998	CAGAAACTAGACAAGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATAT	6057
QY	1561	CGTTTTGACTATCATATCTCTTTGTTTTGTTGATACCTTAGCTGATTTCTAGCATGCTACCT	1620
Db	6058	CGTTTTGACTATCATATCTCTTTGTTTTGTTGATACCTTAGCTGATTTCTAGCATGCTACCT	6117
QY	1621	AATGTACAAAGCAAAAGCGCAACAAAAACCTTATTTATGGCTTGGGAATAATACTCTAGA	1680
Db	6118	AATGTACAAAGCAAAAGCGCAACAAAAACCTTATTTATGGCTTGGGAATAATACTCTAGA	6177
QY	1681	TCAGATGAGAGCCACTACAAAAATGTGAACAAGATGAGGAACGAAGGTTTCCCTAATAG	1740
Db	6178	TCAGATGAGAGCCACTACAAAAATGTGAACAAGATGAGGAACGAAGGTTTCCCTAATAG	6237
QY	1741	TAATTTTGTGTAAGGTTCTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAAAATACCGGT	1800
Db	6238	TAATTTTGTGTAAGGTTCTGTAGTCTGTCAAGTTCAAGAGATTAAAGAAAAAATACCGGT	6297
QY	1801	TGTAGATGACCAAGGACGATATACGGGTAGAACCGGTAAAGAGAGGCGCCCTCAATTC	1860
Db	6298	TGTAGATGACCAAGGACGATATACGGGTAGAACCGGTAAAGAGAGGCGCCCTCAATTC	6357
QY	1861	GAGCAGGCTTCACAACCTCCGTTCTACCGCTTACCAGCAACAGTCCCTCAATCATGGAC	1920
Db	6358	GAGCAGGCTTCACAACCTCCGTTCTACCGCTTACCAGCAACAGTCCCTCAATCATGGAC	6417
QY	1921	CGCGCGTTAGCACAAGTTCGGTTAGAGAATGATGAAGAGAGGCAAAAAATACATGGCGC	1980
Db	6418	CGCGCGTTAGCACAAGTTCGGTTAGAGAATGATGAAGAGAGGCAAAAAATACATGGCGC	6477
QY	1981	TTGATATTCGGGATTGCAATCTTATTTCTTAAACAGTAGTGACCTTGCTGCTATATCTGTAGCC	2040
Db	6478	TTGATATTCGGGATTGCAATCTTATTTCTTAAACAGTAGTGACCTTGCTGCTATATCTGTAGCC	6537
QY	2041	TCCTTTTATATAGCATGAGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG	2100
Db	6538	TCCTTTTATATAGCATGAGGGGCTAGCACACCTAGCGATCTTGTAGGCATACCGACTAGG	6597
QY	2101	ATTTCAGGCGCAGAGAAAAGATTACATCTACACTTTGGTTCCAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCAGGCGCAGAGAAAAGATTACATCTACACTTTGGTTCCAATCAAGATGTAGTAGAT	6657
QY	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTGAGACACA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTGAGACACA	6717
QY	2221	ATTATGAAACGCAATAACATCTCTCTTATCAGATTAAATGGAGCTGCAACCAACAGTGGG	2280
Db	6718	ATTATGAAACGCAATAACATCTCTCTTATCAGATTAAATGGAGCTGCAACCAACAGTGGG	6777
QY	2281	TGGGGGCACTTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	2340
Db	6778	TGGGGGCACTTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	6837
QY	2341	GATGATGCTAGTGCATCATCATCTCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	2400
Db	6838	GATGATGCTAGTGCATCATCATCTCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	6897
QY	2401	ATCCCGGCGCCTACTACAGGATCAGTTGCACTCGAATACCTCTCATTTGACATGAGTGT	2460
Db	6898	ATCCCGGCGCCTACTACAGGATCAGTTGCACTCGAATACCTCTCATTTGACATGAGTGT	6957
QY	2461	ACCATTTACTGTACACCCATTAATGTCTGGATGAGAGATCACTCACATTC	2520
Db	6958	ACCATTTACTGTACACCCATTAATGTCTGGATGAGAGATCACTCACATTC	7017
QY	2521	TATCAGTATTTAGCACTTGTGTGCTCCGCAATCTGCAACAGGGAGGGTATTTCTTTCT	2580

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Db 7018 TATCAGTATTAGACATTGGTGTCTCGGACATCTGCACAGGAGGTATCTTTCT 7077
Qy 2581 ACTCTGGCTTCCATCAACTCGGAGACACCCAAATCGGAAGTCTTGAGTGTGAGTGA 2640
Db 7078 ACTCTGGCTTCCATCAACTCGGAGACACCCAAATCGGAAGTCTTGAGTGTGAGTGA 7137
Qy 2641 ACTCCCTGGGTTGTATATCTGTCTGCGAAAGTACGCGAGACAGAGGAAGAAGATTAT 2700
Db 7138 ACTCCCTGGGTTGTATATCTGTCTGCGAAAGTACGCGAGACAGAGGAAGAAGATTAT 7197
Qy 2701 AACTCAGCTGCCCTACGCGATGTTATCATCGGAGGTTAGGTTTCGAGCGGCAGTACCAC 2760
Db 7198 AACTCAGCTGCCCTACGCGATGTTATCATCGGAGGTTAGGTTTCGAGCGGCAGTACCAC 7257
Qy 2761 GAAAGGACCTPAGATGTACAACTATTTCGGGGAAGTGGGTGGCCAACTACCCAGGAGTA 2820
Db 7258 GAAAGGACCTPAGATGTACAACTATTTCGGGGAAGTGGGTGGCCAACTACCCAGGAGTA 7317
Qy 2821 GGGGGTGGATCTTTATTTGACAGCGCGGTATGGTTCTCAGTCTACGAGGTTTAAACCC 2880
Db 7318 GGGGGTGGATCTTTATTTGACAGCGCGGTATGGTTCTCAGTCTACGAGGTTTAAACCC 7377
Qy 2881 AATTCAACCCAGTACACTGTACAGGAGGAAATATGTATATCAAGCGATACAATGAC 2940
Db 7378 AATTCAACCCAGTACACTGTACAGGAGGAAATATGTATATCAAGCGATACAATGAC 7437
Qy 2941 ACATGCCCAGATGAGCAAGACTACAGATTCGAATGGCCAACTCTTCGTATTAAGCCCTGA 3000
Db 7438 ACATGCCCAGATGAGCAAGACTACAGATTCGAATGGCCAACTCTTCGTATTAAGCCCTGA 7497
Qy 3001 CGGTTTGGTGGAAACCGCATACAGAGCTATCTTATCAAGGTGTCAACATCTTTA 3060
Db 7498 CGGTTTGGTGGAAACCGCATACAGAGCTATCTTATCAAGGTGTCAACATCTTTA 7557
Qy 3061 GGGCAAGACCGGTACTGACTGTACCGCCCAACAGCTACACATCATGGGGCGGAAGGC 3120
Db 7558 GGGCAAGACCGGTACTGACTGTACCGCCCAACAGCTACACATCATGGGGCGGAAGGC 7617
Qy 3121 AGAATCTCAGATAGGAGACTCATCTTCTGTATCAACAGGGTCAATCATCTCTCT 3180
Db 7618 AGAATCTCAGATAGGAGACTCATCTTCTGTATCAACAGGGTCAATCATCTCTCT 7677
Qy 3181 CCCCGTTATTATCTTATGACAGTACAGCAACAAACAGCCACTCTTCTATAGTCTTAT 3240
Db 7678 CCCCGTTATTATCTTATGACAGTACAGCAACAAACAGCCACTCTTCTATAGTCTTAT 7737
Qy 3241 ACATTCAATGCTTCACTCGGCGAGGTAGTATCCCTTGGCGAGCTTCAGCAAGATGCC 3300
Db 7738 ACATTCAATGCTTCACTCGGCGAGGTAGTATCCCTTGGCGAGCTTCAGCAAGATGCC 7797
Qy 3301 AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAAC 3358
Db 7798 AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAAC 7855
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RESULT 2

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5310678-2
; Patent No. 5310678
; APPLICANT: Bingham, Richard W.; Chambers, Phillip; Emmerson, Peter
; T.; Millar, Neil S.
; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/438,945
; FILING DATE: 17-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 885,765
; FILING DATE: 15-JUL-1986
; SEQ ID NO: 2
; LENGTH: 3825
5310678-2
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Query Match 95.2%; Score 3196.4; DB 6; Length 3825;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 1 ACGGGTAGAAGATTCTCGATCCCGGTTGGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
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Qy 61 TTCTACCAAGAACCCAGCACTATGATGCTGATATCCGGTTCGCGTTCGCTGAGTGTG 120
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Qy 121 CATCTGTCCGGCAAACTCCATTCATGATGCGAGCCCTTCGAGGCTTCGAGAAATTTGGTAA 180
Db 121 CATCTGTCCGGCAAACTCCATTCATGATGCGAGCCCTTCGAGGCTTCGAGAAATTTGGTAA 180
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Db 301 CAGGACATTGACCACTTTGCTCACCCCTTGGTACTCTATCCGTAGGTACAGAGTC 360
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Db 361 TGTGACTACATCTGGAGGGGAGACAGGGCGCTTATAGGCGCCATTTAGGCGGTGT 420
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Db 901 ACAGGTAACCTACCTTCAGTCGGGAACCTAAATAATATGCGTCCACCTACTTTGGAAAC 960
Qy 961 CTTATCCGTAAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGTGACACA 1020
Db 961 CTTATCTGTAAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGTGACACA 1020
Qy 1021 GGTGGTCTGTGTATAGAAAGACTTGACACCTCATACTGTATAGAAAGACTGACTTAGATT 1080
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Db	1021	GGTCCGGTTCGTGTAGTAAGAACTTGCACCTCATATTTGTATAGAAACCGCACTTGGA	1080
Qy	1081	ATATTGTACAAGAAATAGTAACGTTCCCTATGTCTCCCTCGGTATTTATTCCTGCTTGAGCGG	1140
Db	1081	ATATTGTACAAGAAATAGTAACATTCCTATGTCTCCCTCGGTATTTATTCCTGCTTGAGCGG	1140
Qy	1141	CAATACGTCGGCCTGTATGTACTCAAAAGACGGAAGCGCACTTACTACACCATACATGAC	1200
Db	1141	CAATACATCGGCCTGTATGTACTCAAAAGACGGAAGCGCACTCACTACGCCATACATGAC	1200
Qy	1201	TATCAAAAGGTTCACTCATCGGCAACTCGAAGATGACAAACATGTAGATGTGTAAACCCGCC	1260
Db	1201	TATCAAAAGGCTCAGTCATCGCTACTCAAGATGACAACATGTAGATGTGTAAACCCGCC	1260
Qy	1261	GGGTATCATATCGCAAAACTATGAGAAGCGGTCTCTTAATAGATAAAACAATCATGCAA	1320
Db	1261	GGGTATCATATCGCAAAACTATGAGAAGCGGTCTCTTAATAGATNAGCAATCATGCAA	1320
Qy	1321	TGTTTTTATCCTTAGCGGGATAACTTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
Db	1321	TGTTTTTATCCTTAGACGGATAACTTTAAGGCTCAGTGGGGAATTCGATGCAACTTATCA	1380
Qy	1381	GAAGAAATATCTCAATAACAAGATTCCTCAAGTAATAAACAAGCAATCTTGATATCTCAAC	1440
Db	1381	GAAGAAATATCTCAATAACAAGATTCCTCAAGTAATAAACAAGCAATCTTGATATCTCAAC	1440
Qy	1441	TGAGCTTGGGAATGTCACAACTCGATCAGTAATGCTTTCAATAAGTTAGAGAAAGCAA	1500
Db	1441	TGAGCTTGGGAATGTCACAACTCGATCAGTAATGCTTTCAATAAGTTAGAGAAAGCAA	1500
Qy	1501	CAGAAAACCTAGACAAAGTCAATGTCAAACCTGACTAGCACATCTGCTCTCATTAACCTATAT	1560
Db	1501	CAGCAAACTAGACAAAGTCAATGTCAAACCTGACCAGCACATCTGCTCTCATTAACCTATAT	1560
Qy	1561	CGTTTTGCACTATCATATCTCTTGTTTTTGGTATATCTTAGCCTGATTTCTAGCATGCTACCT	1620
Db	1561	CGTTTTGCACTATCATATCTCTTGTTTTTGGTATATCTTAGCCTGATTTCTAGCATGCTACCT	1620
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Db	1621	AATGTATAAGCAAAAGCGCAACAAAAGACCTTATTTATGCTTGGGAATAATACTCTAGA	1680
Qy	1681	TCAGATGAGAGCCACTCAAAAATGTGAAACACAGATGAGGAAACGAAGGTTTCCCTAATAG	1740
Db	1681	TCAGATGAGAGCCACTCAAAAATGTGAAACACAGATGAGGAAACGAAGGTTATCCCTAATAG	1740
Qy	1741	TAATTTGTGTGAAAGTTCTGGTAGTCTGTGCAGTTTCAGAGATTAAGAAAAAACTACCGGT	1800
Db	1741	TAATTTGTGTGAAAGTTCTGGTAGTCTGTCAAATTCGGAGAGTTTAGAAAAAACTACCGGT	1800
Qy	1801	TGTAGATGACCAAGAGACGATATACGGGTAGAACGGTTAAGAGAGCGCCCTCAATTGC	1860
Db	1801	TGTAGATGACCAAGAGACGATATACGGGTAGAACGGTTAAGAGAGCGCCCTCAATTGC	1860
Qy	1861	GAGCCAGGCTTCACAACTCCGTTCTACCGCTTCACCGCAACAGTCCTCAATCATGGAC	1920
Db	1861	GAGCCGGGCTTCACAACTCGTTCTACCGCTTCACCGCAGCAGTCCTCAGTCATGGAC	1920
Qy	1921	CGCGCCGTTAGCCAAAGTTGCGTTAGAGAAATGATGAAAGAGAGGCAAAAAATACATGGCGC	1980
Db	1921	CGCGCAGTTAGCCAAAGTTGCGTTAGAGAAATGATGAAAGAGAGGCAAAAAATACATGGCGC	1980
Qy	1981	TTGATATTCGGATTTGCAATCTTATCTTAACAGTAGTAGACCTTGGCTATATCTGTAGCC	2040
Db	1981	TTGATATTCGGGATTTGCAATCTTACTCTTAACAGTAGTAGACCTTGTAGCTACATCTGTAGCC	2040
Qy	2041	TCCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTCTGTAGGCATACCGACTAGG	2100
Db	2041	TCCCTTTGTATATAGCATTGGGGCTAGCACACCTTAGCGACCTTGTAGGCATACCGACGAGG	2100
Qy	2101	ATTTCCAGGGCAGAAAGAAAGATTATCATCTCACTCTGTTTCCAATCAAGATGTAGTAGAT	2160

Qy 3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATCCCTTGGCCAGGCTTCAGCAAGATGCCCC 3300
Db |||||
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Qy 3301 AACTCGTGTGTTACTGGAGTCTATACAGATCCATATCCCTAACTTCTATAGAAACC 3358
Db |||||
Db 3301 AACTCGTGTGTTACTGGAGTCTATACAGATCCATATCCCTAACTTCTATAGAAACC 3358
RESULT 3
5310678-2
; Patent No. 5310678
; APPLICANT: Bingham, Richard W.; Chambers, Philip; Emmerson, Peter
; T.; Millar, Neil S.
; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/438,945
; FILING DATE: 17-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 885,765
; FILING DATE: 15-JUL-1986
; SEQ ID NO: 2:
; LENGTH: 3825
5310678-2
Query Match 95.2%; Score 3196.4; DB 6; Length 3825;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3257; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
Qy 1 ACGGGTGAAGATCTTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Db |||||
Db 1 ACGGGTGAAGATCTTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Qy 61 TTCTACCAAGAACCCAGCACTATGATGCTGACTATCGGGTTGGCTGGCAGTGGTTG 120
Db |||||
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Db |||||
Db 121 CATCTGTCGGCAAACTCCATTGATGGCAGCCCTTTCGCGCTCGAGCAATTGGGTAC 180
Qy 181 AGGAGACAAAGCCGCTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240
Db |||||
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Db 781 TATGGATTACTTGTGACTAAGTTAGGTGTAGGAAACAATCAACTCAGCTCATTAATTCGG 840
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2761 GAAAAGGACCTAGACGCTCAACAATTTATTTGAGGACTGGGTGGCCAACTACCCAGGAGTA 2820
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2821 GGGGTGGATCTTTTATTGACAGCCCGTATGGTTCTCTAGTCTTACGAGGGTTAAAAACC 2880
2881 AATTCAACCAGTGAACACTGTGTACAGGAAGGAATATGTATATACAAGCGATACATGAC 2940
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2941 ACATGCCAGATGAGCAAGACTACAGATTCCGAATGGCCAAAGTCTTTCGTATAGCCCGG 3000
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3121 AGAATTTCTCACAGTAGGGACATCTCAATTTCTTGTATCAGGAGGTCATCATCTTCTCT 3180
3181 CCGCGCTTATTTATCTCTATGACAGTCAGCAACAAACAGCCACTCTTTCATAGTCCCTTAT 3240
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3241 ACATTCATAGCTTCACTCGCCAGGATGATATCCCTTGGCAGGCTTCAGCAAGATGCCCC 3300
3241 ACATTCATAGCTTCACTCGCCAGGATGATATCCCTTGGCAGGCTTCAGCAAGATGCCCC 3300
3301 AACTCGTGTGTACTGAGGTCATATCAGATCCATATCCCTTATCTTATAGAAACC 3358
3301 AACTCGTGTGTACTGAGGTCATATCAGATCCATATCCCTTATCTTATAGAAACC 3358
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RESULT 4

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US-08-484-575A-12
; Sequence 12, Application US/08484575A
; Patent No. 5925358
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran and David E. Junker
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,575A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0450
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 115..1860
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 2095..3756
US-08-484-575A-12

Query Match
Best Local Similarity 98.8%; Score 1741.8; DB 2; Length 4177;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGTCCAGACCTTCTACCAAGAACCC 75
Db TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGTCCAGACCTTCTACCAAGAACCC 2123

Qy 76 AGCACCTATGATGCTGACTATCCGGGTTGGCTGGCACTGAGTTGCACTCTGTCGGGCAA 135
Db AGCACCTATGATGCTGACTATCCGGGTTGGCTGGCACTGAGTTGCACTCTGTCGGGCAA 2183

Qy 136 CTCATTGATGGCAGGCTCTTTCAGCTGCAAGAAATTGGTTACAGAGACAAAGCCGT 195
Db CTCATTGATGGCAGGCTCTTTCAGCTGCAAGAAATTGGTTACAGAGACAAAGCAGT 2243

Qy 196 CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGTCTCTCCGAACTCGCC 255
Db CAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGTCTCTCCGAACTCGCC 2303

Qy 256 CAAGGATAAGAGGCGATGTCGAAAGCCCTTGGATGCAATCAACAGGACATTGACCA 315
Db CAAGGATAAGAGGCGATGTCGAAAGCCCTTGGATGCAATCAACAGGACATTGACCA 2363

Qy 316 TTTGCTCACCCCTTGGTGACTCTATCCGAGGATCAAGAGTCTGACTACATCTGG 375
Db TTTGCTCACCCCTTGGTGACTCTATCCGAGGATCAAGAGTCTGACTACATCTGG 2423

Qy 376 AGGGGGGAGACAGGGGGCCCTTATAGGCGCCATTATTGGCGGTGGCTCTTTGGGGTGC 435
Db AGGGGGGAGACAGGGGGCCCTTATAGGCGCCATTATTGGCGGTGGCTCTTTGGGGTGC 2483

Qy 436 AACTGCGGCAAAATAACAGGGCGGCGAGTCTGATACAGCCAAACAAATGCTGCCAA 495
Db AACTGCGGCAAAATAACAGGGCGGCGAGTCTGATACAGCCAAACAAATGCTGCCAA 2543

Qy 496 CATCCTCGACTTAAGAGAGCATTTGGCGCAACCAATGAGGCTGTGATGAGGTCACTGA 555
Db CATCCTCGACTTAAGAGAGCATTTGGCGCAACCAATGAGGCTGTGATGAGGTCACTGA 2603

Qy 556 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGTGTGTTAATGACCAATT 615
Db CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGTGTGTTAATGACCAATT 2663

Qy 616 TAATAAACAGCTCAGGAATTAGACTGATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 675
Db TAATAAACAGCTCAGGAATTAGACTGATCAAAATTTGCACAGCAAGTTGGTGTAGAGCT 2723

Qy 676 CAACCTGTACTACCAATTTGACTACAGTATTCGGACCAACATCACTTCACCTGCTTT 735
Db CAACCTGTACTACCAATTTGACTACAGTATTCGGACCAACATCACTTCACCTGCTTT 2783

Qy 736 AAACAAGCTGACTATTTCAGGCATTTTAACTAGCTGGTGGAAATATGGATTACTTATT 795
Db AAACAAGCTGACTATTTCAGGCATTTTAACTAGCTGGTGGAAATATGGATTACTTATT 2843

Qy 796 GACTAAGTTAGGTAGGGAAACAATCACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 855
Db GACTAAGTTAGGTAGGGAAACAATCACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 2903

Qy 856 CGGTAAACCTATTCTATACGACTACAGACTCACTCTTGGGTATACAGGTAACTTACC 915
Db CGGTAAACCTATTCTATACGACTACAGACTCACTCTTGGGTATACAGGTAACTTACC 2963

RESULT 5

US-08-477-459-12

; Sequence 12, Application US/08477459

; Patent No. 6001369

; GENERAL INFORMATION:

; APPLICANT: Mark D. Cochran

; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

Qy 916 TTCACTCGGGAACCTTAAATTAATATGCGTGCACCTACTTGGAAACCTTATCCGTAAGCAC 975
Db TTCACTCGGGAACCTTAAATTAATATGCGTGCACCTACTTGGAAACCTTATCCGTAAGCAC 3023

Qy 976 AACACAGGGGATTTGCGTCCGGCCTTTGTCGCCAAAGTGGTGACACAGGTCCGTTCTGTGAT 1035
Db AACACAGGGGATTTGCGTCCGGCCTTTGTCGCCAAAGTGGTGACACAGGTCCGTTCTGTGAT 3083

Qy 1036 AGAAGAACTTGACACCTCATATGTTATAGAACTGACTTAGATTTATATTGTACAAGAAT 1095
Db AGAAGAACTTGACACCTCATATGTTATAGAACTGACTTAGATTTATATTGTACAAGAAT 3143

Qy 1096 AGTAAAGTTCCTTATGTCCTCCCTGGTATTATTCCTGCTTGGCGGCAATACGTCGGCTG 1155
Db AGTAAAGTTCCTTATGTCCTCCCTGGTATTATTCCTGCTTGGCGGCAATACATCGGCTG 3203

Qy 1156 TATGTACTCAAGACCGAAGCGCCTTACTACACCATATGACTATCAAAAGTTTCAGT 1215
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Qy 1216 CATCGCCAACTGCAAGATGACAACTGTAGATGTGTAACCCCGGGTATCATATCGCA 1275
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Qy 1276 AAATATGGAAGCGCGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
Db AAATATGGAAGCGCGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 3383

Qy 1336 CGGGTAACCTTTAAGGCTCAGTGGGAAATTCGATGTAACCTTATCAGAAAGATATCTCAAT 1395
Db CGGGTAACCTTTAAGGCTCAGTGGGAAATTCGATGTAACCTTATCAGAAAGATATCTCAAT 3443

Qy 1396 ACAAGATTCTCAAGTAATAATAACAGGCAATCTTTGATATCTCAACTGAGCTTGGGAATGT 1455
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Qy 1456 CAACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAACTAGACAA 1515
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Db AGTCAATGTCAAACTGACTAGCACATCTGCTCATTTACCTATATATCGTTTGTACTATCAT 3623

Qy 1576 ATCTTGTGTTTGGTATAGCTTACCTGATTTAGCATGTCTACCTAATGTACAGCAAAA 1635
Db ATCTTGTGTTTGGTATAGCTTACCTGATTTAGCATGTCTACCTAATGTACAGCAAAA 3683

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Qy 1696 TACAAAAATGTGACACAGATGAGGACGAGGTTCCCTTAATAGTAATTTTGTGTGAAG 1755
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Qy 1756 TTCTGGTAGTCTGTGCTCAGAGAGTTAAGAAAAA 1792
Db TTCTGGTAGTCTGTGCTCAGAGAGTTAAGAAAAA 3840

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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,459
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 115..1860
FEATURE:
NAME/KEY: CDS
LOCATION: 2095..3756
US-08-477-459-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TGGATCCCGGTGGCGCCCTCCAGGTGCAAGTGGGCTCAGACCTTCTACCAAGAACCC 75
Db 2064 TCGATCCCGGTGGCGCCCTCCAGGTGCAAGTGGGCTCAGACCTTCTACCAAGAACCC 2123

QY 76 AGACCTATGATGCTGACTATCCGGGTGGCTGGCACTCAGTTGGATCTGTCCGCGCAA 135
Db 2124 AGACCTATGATGCTGACTATCCGGGTGGCTGGCACTCAGTTGGATCTGTCCGCGCAA 2183

QY 136 CTCATTGTATGGCAGGCGCTCTTGAGCTGCAGGAAATTGTGGTTACAGGAGACAAAGCCGT 195
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QY 196 CAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCTCTCCCGAATCTGCC 255
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QY 256 CRAGGATAAGAGGCGATGTCGGAAGCCCTTGGATGCATCAACAGGACATTGACCAC 315
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QY 316 TTTGCTCACCCCTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 375
Db 2364 TTTGCTCACCCCTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 2423

QY 376 AGGGGGAGACAGGGCGCCCTTATAGCGCCATTTATGGCGGTGTGGCTCTGGGGTGC 435
Db 2424 AGGGGGAGACAGGGCGCCCTTATAGCGCCATTTATGGCGGTGTGGCTCTGGGGTGC 2483

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QY 496 CATCCTCCGACTTAAAGAGAGCAATTGCGGCAACCAATGAGGCTGTGCATGAGTCACTGA 555
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1036 AGAAGAACTTGACACCTCATACTGTATAGAAACTGACTTAGATTATATGTATCAAGAAT 1095
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3084 AGAAGAACTTGACACCTCATACTGTATAGAAACTGACTTAGATTATATGTATCAAGAAT 3143
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1096 AGTAAAGTTCCCTATGTGTCCTGTTTATTTCTGCTTGGCGGCAATACATCGGCGCTG 1155
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3144 AGTAAAGTTCCCTATGTGTCCTGTTTATTTCTGCTTGGCGGCAATACATCGGCGCTG 3203
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1156 TATGTACTCAAAAGACCGAAGGCGCACTTACTACACCATACATACATCAAAAGTTTCACT 1215
Db
3204 TATGTACTCAAAAGACCGAAGGCGCACTTACTACACCATATATGACTATCAAAAGGCTCAGT 3263
QY
1216 CATCGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCGCGGTATCATATCGCA 1275
Db
3264 CATCGCAACTGCAAGATGACAAACATGTAGATGTGTAAACCCCGCGGTATCATATCGCA 3323
QY
1276 AACTATGAGAGCGCGTCTCTTAATAGATAAAACAATCATCAATGTTTATCCTTAGG 1335
Db
3324 AACTATGAGAGCGCGTCTCTTAATAGATAAAACAATCATCAATGTTTATCCTTAGG 3383
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1336 CGGGATAAATTTAAAGGCTCAGTGGGAAATTCGATGTAACTTATCAAGAAGAAATCTCAAT 1395
Db
3384 CGGGATAAATTTAAAGGCTCAGTGGGAAATTCGATGTAACTTATCAAGAAGAAATCTCAAT 3443
QY
1396 ACAAGATTCTCAAGTAAATAAACAGGCAATCTTGTATATCTCAACTGAGCTTGGGAATGT 1455
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3444 ACAAGATTCTCAAGTAAATAAACAGGCAATCTTGTATATCTCAACTGAGCTTGGGAATGT 3503
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1456 CAAACAATCGATCAGTAATGCTTTGTAATAGTTAGGGAAGCAACAGAAAACCTAGACAA 1515
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3504 CAAACAATCGATCAGTAATGCTTTGTAATAGTTAGGGAAGCAACAGAAAACCTAGACAA 3563
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3564 AGTCAATGTCAAACTCAGTACAGACATCTGCTCTCATTACCTATATCTGTTTGTACTATCAT 3623
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1576 ATCTCTGTTTGTGGTATCTTAGGCTGATCTTAGCATGCTACCTAATGTACAAGCAAAA 1635
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Db 3684 GGCCCAACAAAAACCTTATATGCTTGGGAATAAATACTTAGATCAGATGAGAGCCAC 3743
Qy 1696 TACAAAAATGGAACACAGATGAGGAAGGTTTCCCTAATAGTAATTTGTGTGAAG 1755
Db 3744 TACAAAAATGGAACACAGATGAGGAAGGTTTCCCTAATAGTAATTTGTGTGAAG 3803
Qy 1756 TTCTGGTAGTCTGTGAGTTCAGAGAGGTTAAGAAAAA 1792
Db 3804 TTCTGGTAGTCTGTGAGTTCAGAGAGGTTAAGAAAAA 3840

RESULT 6
US-08-479-869-12
; Sequence 12, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-PEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
US-08-479-869-12

Query Match 51.9%; Score 1741.8; DB 3; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGAGCTTCTTACCAGAACCC 75
Db 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGAGCTTCTTACCAGAACCC 2123

Qy 76 AGCACTTATGATGCTGACTATCCGGTTGCGCTGGCACTCAGTTGCATCTGTCCGCAAA 135
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Db 2244 CAACATATACACCTCATCCAGACAGGATCAATCATATAGTTAAAGCTCTCCCGAATCTGCC 2303
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Qy 1096 AGTAAACGTTCCCTATGTCCCTCGTATTTATTTCTGCTGAGGGGCAATACGTCCGCTG 1155
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Qy 1096 AGTAACGTCCTATGTCCTCCCTGTTATTTATCTCTGCTTGAGCGCAATACGTGGCCTG 1155
Db 3144 AGTAACGTCCTATGTCCTCCCTGTTATTTATCTCTGCTTGAGCGCAATACATCGGCCTG 3203
Qy 1156 TATGTACTCAAGACCGAAGCGGCACCTTACTACACCATATCATGACTATCAAGGTTTCAGT 1215
Db 3204 TATGTACTCAAGACCGAAGCGGCACCTTACTACACCATATCATGACTATCAAGGCTCAGT 3263
Qy 1216 CATGCCAATCTCAAGATGACAAATGTAGATGTGTAAACCCCGCGGTATCATATCGCA 1275
Db 3264 CATGCCAATCTCAAGATGACAAATGTAGATGTGTAAACCCCGCGGTATCATATCGCA 3323
Qy 1276 AACTATGGAAGACCGCTGCTCTTAATAGATAAACAATCATGCAATCTTTATCTCTTAGG 1335
Db 3324 AACTATGGAAGACCGCTGCTCTTAATAGATAAACAATCATGCAATCTTTATCTCTTAGG 3383
Qy 1336 CGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAGAATAATCTCAAT 1395
Db 3384 CGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAGAATAATCTCAAT 3443
Qy 1396 ACAAGATCTCAAGTAATAATAACAGGCAATCTTTGATATCTCAACTGAGCTTGGGAATGT 1455
Db 3444 ACAAGATCTCAAGTAATAATAACAGGCAATCTTTGATATCTCAACTGAGCTTGGGAATGT 3503
Qy 1456 CAACAACCTCGATCAGTAAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACCTAGACAA 1515
Db 3504 CAACAACCTCGATCAGTAAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACCTAGACAA 3563
Qy 1516 AGTCAATGTCAAACTGACTAGACATCTGCTCTCAATACCTATATATCGTTTGTGACTATCAT 1575
Db 3564 AGTCAATGTCAAACTGACTAGACATCTGCTCTCAATACCTATATATCGTTTGTGACTATCAT 3623
Qy 1576 ATCTCTTGTGTTTGGTATATCTAGCCTGATTTCTAGCATGCTACCTAATGTACAGCAAAA 1635
Db 3624 ATCTCTTGTGTTTGGTATATCTAGCCTGATTTCTAGCATGCTACCTAATGTACAGCAAAA 3683
Qy 1636 GGCGCAACAAAACCTTATATGCTTGGGAATAATCTAGATCAGATGAGAGCCAC 1695
Db 3684 GGCGCAACAAAACCTTATATGCTTGGGAATAATCTAGATCAGATGAGAGCCAC 3743
Qy 1696 TACAAAATGTGAACAGATGAGGAACGAGGTTTCCCTAATAGTAATTTGTGTGAAG 1755
Db 3744 TACAAAATGTGAACAGATGAGGAACGAGGTTTCCCTAATAGTAATTTGTGTGAAG 3803
Qy 1756 TTCTGGTAGTCTGTCAGTTCAGAGATGTTAAGAAAAA 1792
Db 3804 TTCTGGTAGTCTGTCAGTTCGAGAGTTAAGAAAAA 3840
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RESULT 8

PCT-US94-01826A-12

Sequence 12 Application PC/TUS9401826A

GENERAL INFORMATION:

APPLICANT: Syntro Corporation, et al.

TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01826A

FILING DATE: 28-FEB-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

```
NAME: White Esq. John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
NAME/KEY: CDS
LOCATION: 115..1860
FEATURE:
NAME/KEY: CDS
LOCATION: 2095..3756
PCT-US94-01826A-12
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Query Match 51.9%; Score 1741.8; DB 5; Length 4177;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTTTACCAAGAACCC 75
Db 2064 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTTTACCAAGAACCC 2123
Qy 76 AGACCTATGATCTGACTATCCGGTTGCGCTGCGCACTGAGTTGCACTCTGTCGGCAAA 135
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Db 2364 TTTTGCTCACCCCTTTGGTCACTCTATCCGTAGGATACAGAGTCTCTGACTACATCTGG 2423
Qy 376 AGGGGGAGACAGGGCGCCTTATAGCGGCATTATTGGCGGTGTGGCTCTTGGGGTTGC 435
Db 2424 AGGGGGAGACAGGGCGCCTTATAGCGGCATTATTGGCGGTGTGGCTCTTGGGGTTGC 2483
Qy 436 AACTGCGCAAAATAACAGCGCCGAGCTCTGTATACAGCCAAACAAATGCTGCCAA 495
Db 2484 AACTGCGCAAAATAACAGCGCCGAGCTCTGTATACAGCCAAACAAATGCTGCCAA 2543
Qy 496 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGTCACTGA 555
Db 2544 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGATGAGTCACTGA 2603
Qy 556 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGTCTTGTATGACCAATT 615
Db 2604 CGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGTCTTGTATGACCAATT 2663
Qy 616 TAATAAAACAGCTCAGGAATTAGATGTCATCAAAATTTGCAAGCAAGTTGGTGTAGAGCT 675
Db 2664 TAATAAAACAGCTCAGGAATTAGATGTCATCAAAATTTGCAAGCAAGTTGGTGTAGAGCT 2723
Qy 676 CAACCTGTACTTAACCGAATTGACTACAGTATTTCGGACCAAAATCACTTACCTGCTTT 735
Db 2724 CAACCTGTACTTAACCGAATTGACTACAGTATTTCGGACCAAAATCACTTACCTGCTTT 2783
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QY 736 AAACAAGCTGACTATTGAGCAGCTTTTCAATCTAGCTGGTGGAAATATGGAATTACTATT 795
Db 2784 AAACAAGCTGACTATTGAGCAGCTTTTCAATCTAGCTGGTGGAAATATGGAATTACTATT 2843
QY 796 GACTAAGTTAGGTAGGGAACAATCACTAGCTCAATTAATCGGTAGCGGCTTAATCAC 855
Db 2844 GACTAAGTTAGGTATAGGGAACAATCACTAGCTCAATTAATCGGTAGCGGCTTAATCAC 2903
QY 856 CGGTAACCCCTATTCTATAGACTACAGACTCAACTCTGGGTATACAGTAACCTTACC 915
Db 2904 CGGTAACCCCTATTCTATAGACTACAGACTCAACTCTGGGTATACAGTAACCTTACC 2963
QY 916 TTCAAGTCGGGAACCTAAATAATATGCGTGCACCTACTTTGGAAACCTTATCGTAAAGCAC 975
Db 2964 TTCAAGTCGGGAACCTAAATAATATGCGTGCACCTACTTTGGAAACCTTATCGTAAAGCAC 3023
QY 976 AACCGGGGATTTGCCCTCGGCACTTGTCCAAAAGTGGTGACACAGTGGTCTGTGAT 1035
Db 3024 AACCGGGGATTTGCCCTCGGCACTTGTCCAAAAGTGGTGACACAGTGGTCTGTGAT 3083
QY 1036 AGAAGAACTTGACACCTCATCTACTGTATAGAACTGACTTAGATTTATATTGTACAGAAT 1095
Db 3084 AGAAGAACTTGACACCTCATCTACTGTATAGAACTGACTTAGATTTATATTGTACAGAAT 3143
QY 1096 AGTAACGTTCCCTATGTCCTCGCTGATTTATTTCTGCTTGAGCGGCAATACGTCGCCCTG 1155
Db 3144 AGTAACGTTCCCTATGTCCTCGCTGATTTATTTCTGCTTGAGCGGCAATACATCGGCCCTG 3203
QY 1156 TATGTACTCAAGACCGAAGGCGCACTTACTACCAATCATGACTATCAAGGTTTCAGT 1215
Db 3204 TATGTACTCAAGACCGAAGGCGCACTTACTACCAATCATGACTATCAAGGTTTCAGT 3263
QY 1216 CATCGGCACTCAAGATGACACATGATAGTGTAAACCCCGGGTATCATATCGCA 1275
Db 3264 CATCGGCACTCAAGATGACACATGATAGTGTAAACCCCGGGTATCATATCGCA 3323
QY 1276 AAACATGAGGAAGCGGTGCTCTAATAGATAAACAATCATGCAATGTTTTATCTCTAGG 1335
Db 3324 AAACATGAGGAAGCGGTGCTCTAATAGATAAACAATCATGCAATGTTTTATCTTAGG 3383
QY 1336 CGGGAATCTTTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCAAGAAATCTCAAT 1395
Db 3384 CGGGAATCTTTAAGGCTCAGTGGGGAATTCGATGTAATCTTATCAAGAAATCTCAAT 3443
QY 1396 ACAAGATCTCAAGTAATATACAGCAATCTTGATATCTCAATGAGCTTGGGAATGT 1455
Db 3444 ACAAGATCTCAAGTAATATACAGCAATCTTGATATCTCAATGAGCTTGGGAATGT 3503
QY 1456 CAACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA 1515
Db 3504 CAACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGGAAGCAACAGAAAACTAGACAA 3563
QY 1516 AGTCAATGCAAACTGACTAGACATCTGCTCTCATTAATCTATATCGTTTTGACTATCAT 1575
Db 3564 AGTCAATGCAAACTGACTAGACATCTGCTCTCATTAATCTATATCGTTTTGACTATCAT 3623
QY 1576 ATCTCTGTTTTGTTGATATCTTAGCTGATTTAGCATGCTAATGTACAGCAAAA 1635
Db 3624 ATCTCTGTTTTGTTGATATCTTAGCTGATTTAGCATGCTAATGTACAGCAAAA 3683
QY 1636 GGGCAACAAAAACCTTATATGCGTGGGAATAATATCTAGATCAGATGAGAGCCAC 1695
Db 3684 GGGCAACAAAAACCTTATATGCGTGGGAATAATATCTAGATCAGATGAGAGCCAC 3743
QY 1696 TACAAAAATGTGAACACAGATAGGAACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG 1755
Db 3744 TACAAAAATGTGAACACAGATAGGAACGAAGGTTTCCCTAATAGTAATTTGTGTGAAG 3803
QY 1756 TTCTGTAGTCTGTGAGTTTCAGAGAGTTAAGAAAAA 1792
Db 3804 TTCTGTAGTCTGTGAGTTTCAGAGAGTTAAGAAAAA 3840

RESULT 9
PCT-US94-02252A-12
; Sequence 12: Application PC/TUS9402252A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02252A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
; PCT-US94-02252A-12
Query Match 51.9%; Score 1741.8; DB 5; Length 4177;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1755; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 16 TGGATCCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
Db 2064 TCGATCCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 2123
QY 76 AGCACCTATGATGCTGACTATCGGGTTCGCTGGCACTGAGTTGCACTGTCCGGCAAA 135
Db 2124 AGCACCTATGATGCTGACTATCGGGTTCGCTGGCACTGAGTTGCACTGTCCGGCAAA 2183
QY 136 CTCCTATTGATGGAGGCTCTTTCGAGCTCGAGGAATTTGGTTACAGGAGACAAAGCCGT 195
Db 2184 CTCCTATTGATGGAGGCTCTTTCGAGCTCGAGGAATTTGGTTACAGGAGACAAAGCAGT 2243
QY 196 CAACATATACCTCATCTCCAGACAGGATCAATAGTTAAGTCTCTCCCGAATCTGCC 255
Db 2244 CAACATATACCTCATCTCCAGACAGGATCAATAGTTAAGTCTCTCCCGAATCTGCC 2303
QY 256 CAAGGATAAGGAGGATGTGCGAAAGCCCCCTTTGGATGATACAAACAGGACATTTGACCAC 315
Db 2304 AAAGGATAAGGAGGATGTGCGAAAGCCCCCTTTGGATGATACAAACAGGACATTTGACCAC 2363
QY 316 TTGTGTCACCCCTTTGGTGTACTCTATCGTAGGATACAAAGAGTCTGTGACTACATCTGG 375

Db 2364 TTTGCTACCCCTTGTGTGACTCTATCCGTAGGATACAAGAGTCTGTGACTACATCTGG 2423
Qy 376 AGGGGGAGACAGGGGCGCCTTATAGGCGCCATTAATGGCGGTGTGGCTCTTGGGGTTC 435
Db 2424 AGGGGGAGACAGGGGCGCCTTATAGGCGCCATTAATGGCGGTGTGGCTCTTGGGGTTC 2483
Qy 436 AACTGCCGCAAAATAACAGGGCGGCGAGCTCTGATACAAAGCCAAACAAAATGCTGCCAA 495
Db 2484 AACTGCCGCAAAATAACAGGGCGGCGAGCTCTGATACAAAGCCAAACAAAATGCTGCCAA 2543
Qy 496 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGCTGTGCAATGAGTCACTGA 555
Db 2544 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGCTGTGCAATGAGTCACTGA 2603
Qy 556 CGGATTAATCGCACTAGCAGTGGCAGTTGGGAAGATGACAGAGTTGTTGTAATGACCAATT 615
Db 2604 CGGATTAATCGCACTAGCAGTGGCAGTTGGGAAGATGACAGAGTTGTTGTAATGACCAATT 2663
Qy 616 TAATAAAACAGCTCAGGNAATTAGACTGCATCAAAATTCACAGCAGTGTGTGAGAGCT 675
Db 2664 TAATAAAACAGCTCAGGNAATTAGACTGCATCAAAATTCACAGCAGTGTGTGAGAGCT 2723
Qy 676 CAACCTGTACCTAACCGAATTTAGCTACAGTATTCGGACCAAAATCACTTCACCTGCTTT 735
Db 2724 CAACCTGTACCTAACCGAATTTAGCTACAGTATTCGGACCAAAATCACTTCACCTGCTTT 2783
Qy 736 AAACAAGCTGACTATTACAGGCACTTTACAATCTAGCTGGTGGAAATATGGAATTAATT 795
Db 2784 AAACAAGCTGACTATTACAGGCACTTTACAATCTAGCTGGTGGAAATATGGAATTAATT 2843
Qy 796 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 855
Db 2844 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCAATTAATCGGTAGCGGCTTAATCAC 2903
Qy 856 CGGTAACCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTACC 915
Db 2904 CGGTAACCTATTCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACCTACC 2963
Qy 916 TTCAGTCGGGAACCTAAATAATATCGGTGCGCACCTACTTGGAAACCTTATCCGTAAGCAC 975
Db 2964 TTCAGTCGGGAACCTAAATAATATCGGTGCGCACCTACTTGGAAACCTTATCCGTAAGCAC 3023
Qy 976 AACAGGGGATTTGCTCGGCACCTTGTCCCAAAAGTGTGACACAGGTCGGTTCGTGAT 1035
Db 3024 AACAGGGGATTTGCTCGGCACCTTGTCCCAAAAGTGTGACACAGGTCGGTTCGTGAT 3083
Qy 1036 AGRAGAATTTGACACCTCATCTGTATAGAACTGACTTAGATTATATTTGTAACAAGAT 1095
Db 3084 AGRAGAATTTGACACCTCATCTGTATAGAACTGACTTAGATTATATTTGTAACAAGAT 3143
Qy 1096 AGTAACGTTCCCTATGTCCTGCTGATTTATTCCTGCTTGAAGCGCAATAGTCGGGCTG 1155
Db 3144 AGTAACGTTCCCTATGTCCTGCTGATTTATTCCTGCTTGAAGCGCAATAGTCGGGCTG 3203
Qy 1156 TATGTACTCAAAGACCGAAGCGGCATTTATACACCATATGATCTATCAAAGTTTCAGT 1215
Db 3204 TATGTACTCAAAGACCGAAGCGGCATTTATACACCATATGATCTATCAAAGTTTCAGT 3263
Qy 1216 CATGCCAATGCAAGATGACAAATGTGTAGATGTGTAAACCCCGGGTATCATATCGCA 1275
Db 3264 CATGCCAATGCAAGATGACAAATGTGTAGATGTGTAAACCCCGGGTATCATATCGCA 3323
Qy 1276 AAATATGGAAGACCGGTGCTCTAAATAGATAAAACAATCATGCAATGTTTTATCCTTAGG 1335
Db 3324 AAATATGGAAGACCGGTGCTCTAAATAGATAAAACAATCATGCAATGTTTTATCCTTAGG 3383
Qy 1336 CGGGATAAATTTAAGGCTCAGTGGGGAAATTCGATGTAACTTTATCAGAAGAAATCTCAAT 1395
Db 3384 CGGGATAAATTTAAGGCTCAGTGGGGAAATTCGATGTAACTTTATCAGAAGAAATCTCAAT 3443
Qy 1396 ACAAGATTTCAAGTAATAATAACAGGCAATCTTTGATATCTCAACTGAGCTTGGGAATGT 1455
Db 3444 ACAAGATTTCAAGTAATAATAACAGGCAATCTTTGATATCTCAACTGAGCTTGGGAATGT 3503

RESULT 10

US-08-663-566A-12

; Sequence 12, Application US/08663566A

; Patent No. 5853733

; GENERAL INFORMATION:

; APPLICANT: Cochran, Mark D

; APPLICANT: Macdonald, Richard D

; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys

; TITLE OF INVENTION: and Uses Thereof

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/663,566A

; FILING DATE: June 13, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P

; REGISTRATION NUMBER: 28,678

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; TELEX: 422523

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1662 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1662

US-08-663-566A-12

Query Match		48.6%;	Score 1631.6;	DB 2;	Length 1662;		
Best Local Similarity		98.9%;	Pred. No. 0;				
Matches 1643;		Conservative	0;	Mismatches	19;	Indels	0;
		Gaps	0;				
QY	47	ATGGGCTCAGACCTTCTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGGTGGC	106				
DB	1	ATGGGCTCAGACCTTCTACCAAGAACCCAGACACCTATGATGCTGACTATCCGGGTGGC	60				
QY	107	CTGGCACTGAGTTGCACTCTGTCGGGCAACTCCATTGATGGCAGGCTCTTGACGTGCA	166				
DB	61	CTGGTACTGAGTTGCACTCTGTCGGGCAACTCCATTGATGGCAGGCTCTTGACGTGCA	120				
QY	167	GGAAATGTGTTACAGAGACAAAGCGCTCAACATATACACCTCATCCACAGACAGGATCA	226				
DB	121	GGAAATGTGTTACAGAGACAAAGCGCTCAACATATACACCTCATCCACAGACAGGATCA	180				
QY	227	ATCATAGTTAAGTCTCTCCGGAATCTGCCAAGGATAAGAGGAGCATGTGCGAAAGCCCC	286				
DB	181	ATCATAGTTAAGTCTCTCCGGAATCTGCCAAGGATAAGAGGAGCATGTGCGAAAGCCCC	240				
QY	287	TTGGATGTCATACACAGGACATTTGACCATTTTGTCTCACCCCTTGGTGACTCTATCCGT	346				
DB	241	TTGGATGTCATACACAGGACATTTGACCATTTTGTCTCACCCCTTGGTGACTCTATCCGT	300				
QY	347	AGGATACAAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCCCTTATAGCGCC	406				
DB	301	AGGATACAAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCCCTTATAGCGCC	360				
QY	407	ATTATTGGGGTGTGGCTCTTGGGGTTGCAACTGGCCGCAAAATAACAGCGGCGCAGCT	466				
DB	361	ATTATTGGGGTGTGGCTCTTGGGGTTGCAACTGGCCGCAAAATAACAGCGGCGCAGCT	420				
QY	467	CTGATACAGCCAAACAAATGCTGCCACATCCTCGACTTAAAGAGGACATTGCGCA	526				
DB	421	CTGATACAGCCAAACAAATGCTGCCACATCCTCGACTTAAAGAGGACATTGCGCA	480				
QY	527	ACCAATGAGGCTGTGATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGG	586				
DB	481	ACCAATGAGGCTGTGATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGG	540				
QY	587	AGATGAGCAGTTTGTATTAATGACCAATTTAATAAAGAGCTCAGGAATTAGACTGCATC	646				
DB	541	AGATGAGCAGTTTGTATTAATGACCAATTTAATAAAGAGCTCAGGAATTAGACTGCATC	600				
QY	647	AAATTTGCACAGCAAGTTGGTGTAGAGCTCAACTGTACCTACCGAATTTGACTACAGTA	706				
DB	601	AAATTTGCACAGCAAGTTGGTGTAGAGCTCAACTGTACCTACCGAATTTGACTACAGTA	660				
QY	707	TTGGGACCAAAATCACTTCACCTGCTTTAAACAAGCTGACTATTGAGGACATTTACAAT	766				
DB	661	TTGGGACCAAAATCACTTCACCTGCTTTAAACAAGCTGACTATTGAGGACATTTACAAT	720				
QY	767	CTAGCTGGTGGAAATATGGATTACTTATTAAGTATGAGTGTAGGGAACAATCAACTC	826				
DB	721	CTAGCTGGTGGAAATATGGATTACTTATTAAGTATGAGTGTAGGGAACAATCAACTC	780				
QY	827	AGCTCATTATCGGTAGCGCTTAATCACCGTAACCTTATTTATACGACTCACAGACT	886				
DB	781	AGCTCATTATCGGTAGCGCTTAATCACCGTAACCTTATTTATACGACTCACAGACT	840				
QY	887	CAACTCTTGGGTATACAGGTAACCTTACCTTCACTGGGAACTTAATATATGCGGTGCC	946				
DB	841	CAACTCTTGGGTATACAGGTAACCTTACCTTCACTGGGAACTTAATATATGCGGTGCC	900				
QY	947	ACTTACTTGGAAACCTTATCCGTAAGCACAAACAGGGGATTTGCCCTGGCACTTGCCCA	1006				
DB	901	ACTTACTTGGAAACCTTATCCGTAAGCACAAACAGGGGATTTGCCCTGGCACTTGCCCA	960				
QY	1007	AAAGTGTGACAGGTCGGTCTGTGATAGAGACTTGACACCTCATACTCTATAGAA	1066				
DB	961	AAAGTGTGACAGGTCGGTCTGTGATAGAGACTTGACACCTCATACTCTATAGAA	1020				
QY	1067	ACTGACTTAGATTTATTTGTAACAAGAAATAGTAACGTTCCCTATGTCCTCGTATTTAT	1126				

DB	1021	ACTGACTTAGATTTATTTATTTGTAACAAGATAGTAACGTTCCCTATGTCCTCGTATTTAC	1080				
QY	1127	TCCTGCTTCAGCGGCAATACGTCGGCTCTGATGCTACTCAAGACCGAAGCGCACCTACT	1186				
DB	1081	TCCTGCTTCAGCGGCAATACATCGGCTCTGATGCTACTCAAGACCGAAGCGCACCTACT	1140				
QY	1187	ACACCATACATGACTATCAAGGTTCAAGTCATCGCCAACTGCAAGATGACAAATGTAGA	1246				
DB	1141	ACACCATATGACTATCAAGGTTCAAGTCATCGCTAACTGCAAGATGACAAATGTAGA	1200				
QY	1247	TGTGTAAACCCCGGCTATCATATCGAAAACTATGGAAGCCCTGCTCTTAATAGAT	1306				
DB	1201	TGTGTAAACCCCGGCTATCATATCGAAAACTATGGAAGCCCTGCTCTTAATAGAT	1260				
QY	1307	AAACATCATGCAATGTTTTATCTTAGGGGGATTAACCTTAAAGGCTCAGTGGGAATTC	1366				
DB	1261	AAACATCATGCAATGTTTTATCTTAGGGGGATTAACCTTAAAGGCTCAGTGGGAATTC	1320				
QY	1367	GATGTAACTTATCAGAAAGATATCTCAATACAAGATTCTCAAGTAATAATAACAGCAAT	1426				
DB	1321	GATGTAACTTATCAGAAAGATATCTCAATACAAGATTCTCAAGTAATAATAACAGCAAT	1380				
QY	1427	CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAG	1486				
DB	1381	CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAG	1440				
QY	1487	TTAGAGGAAGCAACAGAAAACCTAGACAAAGTCAATGTCAAACTGACAGCACATCTGCT	1546				
DB	1441	TTAGAGGAAGCAACAGAAAACCTAGACAAAGTCAATGTCAAACTGACAGCACATCTGCT	1500				
QY	1547	CTCATTACCTATATCTTTTGTACTATCATCTCTTTGTTTGTGTATATCTAGCCTGATT	1606				
DB	1501	CTCATTACCTATATCTTTTGTACTATCATCTCTTTGTTTGTGTATATCTAGCCTGATT	1560				
QY	1607	CTAGCATGTACTAATGTACAAGCAAAAGGCGCAACAAAAACCTTATATGGCTTGGG	1666				
DB	1561	CTAGCATGTACTAATGTACAAGCAAAAGGCGCAACAAAAACCTTATATGGCTTGGG	1620				
QY	1667	ATAATATCTTAGATCAGATGAGGCCACTACAAAAATGTGA	1708				
DB	1621	ATAATATCTTAGATCAGATGAGGCCACTACAAAAATGTGA	1662				

RESULT 11
US-08-023-610-12
; Sequence 12, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; APPLICANT: Macdonald Ph.D, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023.610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1662
US-08-023-610-12

Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCG 106
Db 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGACTATCCGGGTTGCG 60

Qy 107 CTGCGACTGAGTTGCTATGTCGGGCAAACTCCATTGATGGCAGGCTCTTTGCAAGTGA 166
Db 61 CTGCGTACTGAGTTGCTATGTCGGGCAAACTCCATTGATGGCAGGCTCTTTGCAAGTGA 120

Qy 167 GGAATGCTGGTTACAGGAGCAAAAGCGCTCAACATATACACCTCATCCAGAGAGGATCA 226
Db 121 GGAATGCTGGTTACAGGAGCAAAAGCGCTCAACATATACACCTCATCCAGAGAGGATCA 180

Qy 227 ATCATAGTTAAGTCTCTCCGGAATCTGCCAAGGATAAGGAGCATGTGCGAAAGCCCC 286
Db 181 ATCATAGTTAAGTCTCTCCGGAATCTGCCAAGGATAAGGAGCATGTGCGAAAGCCCC 240

Qy 287 TTGATGATCAACAGGACATTTGACCACTTTGCTCAACCCCTTTGCTGATCTTATCCGT 346
Db 241 TTGATGATCAACAGGACATTTGACCACTTTGCTCAACCCCTTTGCTGATCTTATCCGT 300

Qy 347 AGGATACAAGGCTGTGACTACATCTGGAGGGGGAGAGAGGGGCCCTTTATAGGGCC 406
Db 301 AGGATACAAGGCTGTGACTACATCTGGAGGGGGAGAGAGGGGCCCTTTATAGGGCC 360

Qy 407 ATTATTGGCGGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATAACAGCGGCGCAGCT 466
Db 361 ATTATTGGCGGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATAACAGCGGCGCAGCT 420

Qy 467 CTGATACAAGCCAAACAAAATGTGCGCAATCTCCGACTTAAAGAGAGCATTTGCCGCA 526
Db 421 CTGATACAAGCCAAACAAAATGTGCGCAATCTCCGACTTAAAGAGAGCATTTGCCGCA 480

Qy 527 ACCAATGAGCTGTGATGAGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGG 586
Db 481 ACCAATGAGCTGTGATGAGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGG 540

Qy 587 AAGATGAGCAGTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTAGACTGCATC 646
Db 541 AAGATGAGCAGTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTAGACTGCATC 600

Qy 647 AAAATTGCAAGGTTGGTTAGAGCTCAACCTGTACCTTAACCGAAATTTGACTACAGTA 706
Db 601 AAAATTGCAAGGTTGGTTAGAGCTCAACCTGTACCTTAACCGAAATTTGACTACAGTA 660

Qy 707 TTGGGACCAAAATCACTTACCTGCTTTAAACAGCTGACTATTTCAGGCACATTACAAT 766
Db 661 TTGGGACCAAAATCACTTACCTGCTTTAAACAGCTGACTATTTCAGGCACATTACAAT 720

Qy 767 CTAGCTGGTGAATATGGATTACTTATGCTAAGTTAGTGTAGGGAACAATCAACTC 826
Db 721 CTAGCTGGTGAATATGGATTACTTATGCTAAGTTAGTGTAGGGAACAATCAACTC 780

RESULT 12

US-08-288-065A-12
; Sequence 12, Application US/08288065A
; Patent No. 5961982
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
; TITLE OF INVENTION: HVT-050 and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White

Qy 827 AGCTCATTAAATCGGTAGCGGCTTAATCAACCGGTAAACCTATTCTATACGACTCACAGACT 886
Db 781 AGCTCATTAAATCGGTAGCGGCTTAATCAACCGGTAAACCTATTCTATACGACTCACAGACT 840

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Db 1621 AATAATATCTTAGATCAGATGAGAGCCACTTACAAAATGTGA 1662

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/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ FILING DATE: Aug-09-94
/ APPLICATION NUMBER: US/08/288,065A
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)278-0400
/ TELEFAX: (212)391-0526
/ TELEX: 422523
/
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1662 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1662
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/ US-08-288-065A-12
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/ Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
/ Best Local Similarity 98.9%; Pred. No. 0;
/ Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Qy 1667 AATAACTCTAGATCAGATGAGAGCCACTACAAAATGTGA 1708
Db 1621 AATAATACCTAGATCAGATGAGAGCCACTACAAAATGTGA 1662

RESULT 13

US-08-362-240A-12
; Sequence 12, Application US/08362240A
; Patent No. 5965138
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Junker, David
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,240A
; FILING DATE: Dec-22-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-362-240A-12

Query Match 48.6%; Score 1631.6; DB 2; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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QY 1607 CTAGCATGCTACCTAAATGTACAAGCAAAAGCGCAACAAAACCTTATTATGCTTGGG 1666
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Db 1621 AATAAATCTCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1662

RESULT 14

US-08-804-372A-10
; Sequence 10, Application US/08804372A
; Patent No. 6183753
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Wild, Martha A.
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,372A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2552/39115E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-804-372A-10

Query Match 48.6%; Score 1631.6; DB 3; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;

Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 47 ATGGGCTCCAGACCTTTTACCAAGAACCAGACACCTATGATGCTGACTATCCGGGTGCG 106
Db 1 ATGGGCTCCAGACCTTTTACCAAGAACCAGACACCTATGATGCTGACTATCCGGGTGCG 60
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QY 1427 CTTGATATCTCAACTGAGCTTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATAAG 1486
Db 1381 CTTGATATCTCAACTGAGCTTTGGGAATGTCAACAACCTCGATCAGTAATGCTTTGAATAAG 1440
QY 1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCT 1546
Db 1441 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCAATCTGCT 1500
QY 1547 CTCAATACCTATATCGTTTGGACTATCATATCTCTGTTTGGTATACCTTAGCCTGATT 1606
Db 1501 CTCAATACCTATATCGTTTGGACTATCATATCTCTGTTTGGTATACCTTAGCCTGATT 1560
QY 1607 CTAGCATGCTACCTAAATGTACAGCAAAAGCGCAACAAACCTTATTATGCTTGGG 1666
Db 1561 CTAGCATGCTACCTAAATGTACAGCAAAAGCGCAACAAACCTTATTATGCTTGGG 1620
QY 1667 AATAAATCTCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1708
Db 1621 AATAAATCTCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1662

RESULT 15

PCT-US95-10245-12

Sequence 12, Application PC/TUS9510245

GENERAL INFORMATION:

APPLICANT: SYNTRO CORPORATION

TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10245

FILING DATE: 09-AUG-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)278-0400

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TELEX: 422523

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1662
PCT-US95-10245-12

Query Match 48.8%; Score 1631.6; DB 5; Length 1662;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCG 106
Db 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCG 60
QY 107 CTGGCACTGAGTTGCACTCTGTCGGGCAAACTCCATTGATGGCAGGCCCTTTGCAGCTGCA 166
Db 61 CTGGTACTGAGTTGCACTCTGTCGGGCAAACTCCATTGATGGCAGGCCCTTTGCAGCTGCA 120
QY 167 GGAATTGTGGTTACAGAGACAAAGCCGTCAAATATACCTCATCCAGAGAGATCA 226
Db 121 GGAATTGTGGTTACAGAGACAAAGCCGTCAAATATACCTCATCCAGAGAGATCA 180
QY 227 ATCATAGTTAAGTCTCCCGAATCTGCCAAGGATTAAGGAGCATGTGCGAAAGCCCC 286
Db 181 ATCATAGTTAAGTCTCCCGAATCTGCCAAGGATTAAGGAGCATGTGCGAAAGCCCC 240
QY 287 TTGGATGCATACAAAGGACATTTGACCACTTGTCTCACCCCCCTTGTGTGACTCTATCCGT 346
Db 241 TTGGATGCATACAAAGGACATTTGACCACTTGTCTCACCCCCCTTGTGTGACTCTATCCGT 300
QY 347 AGGATACAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCCCTTTATAGGGCC 406
Db 301 AGGATACAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGGGCCCTTTATAGGGCC 360
QY 407 ATTTATGGGGGTGTGGCTCTTGGGTTGCACTGCGCGCAAAATACAGCGGCGCAGCT 466
Db 361 ATTTATGGGGGTGTGGCTCTTGGGTTGCACTGCGCGCAAAATACAGCGGCGCAGCT 420
QY 467 CTGATACAGCCAAACAAATGCTGCCAATCTCGACTTAAAGAGAGCATTTGCCGCA 526
Db 421 CTGATACAGCCAAACAAATGCTGCCAATCTCGACTTAAAGAGAGCATTTGCCGCA 480
QY 527 ACCAATGAGGCTGTGCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGG 586
Db 481 ACCAATGAGGCTGTGCATGAGGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGG 540
QY 587 AAGATGAGCAGTGTGTTAATGACCAATTTAATAAACAGCTCAGGAAATTAGCTGCATC 646
Db 541 AAGATGAGCAGTGTGTTAATGACCAATTTAATAAACAGCTCAGGAAATTAGCTGCATC 600
QY 647 AAAATTGCACAGCAAGTTGGTGTAGAGCTCAACTGTACCTAACCCGAAATTTAGCTACAGTA 706
Db 601 AAAATTGCACAGCAAGTTGGTGTAGAGCTCAACTGTACCTAACCCGAAATTTAGCTACAGTA 660
QY 707 TTCGGACCAAAATCACTTCCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTCAAT 766
Db 661 TTCGGACCAAAATCACTTCCACCTGCTTTAAACAAGCTGACTATTTCAGGCACTTTCAAT 720
QY 767 CTAGCTGGTGGAAATATGATTAATTTGACTTATTTAGCTTAGGTAGGGAACAATCACTC 826
Db 721 CTAGCTGGTGGAAATATGATTAATTTGACTTATTTAGCTTAGGTAGGGAACAATCACTC 780
QY 827 AGCTCATTAATCGGTAGCGGCTTAATCACCGGTAAACCTATTCTATACGACTCACAGACT 886
Db 781 AGCTCATTAATCGGTAGCGGCTTAATCACCGGTAAACCTATTCTATACGACTCACAGACT 840

QY	887	CAACTCTTGGGTATACAGGTAACCTACCTTCAGTCGGGAACCTAAATAATATGCGTGCC	946
Db	841	CAACTCTTGGGTATACAGGTAACCTACCTTCAGTCGGGAACCTAAATAATATGCGTGCC	900
QY	947	ACCTACTTGGAAACCTTATCCGTAAGCAAAACAGGGGATTTGCCCTCGGCACCTTGTCCCA	1006
Db	901	ACCTACTTGGAAACCTTATCCGTAAGCAAAACAGGGGATTTGCCCTCGGCACCTTGTCCCA	960
QY	1007	AAAGTGTGTACACAGGTCGGTCTGTGATAGAAAGCTTGACACACCTCATACTGTATAGAA	1066
Db	961	AAAGTGTGTACACGGGTCGGTCTGTGATAGAAAGCTTGACACCTCATACTGTATAGAA	1020
QY	1067	ACTGACTTAGATTTATATTGTACAAGAATAGTAACGTTCCCTATGTCCTCGGTATTTAT	1126
Db	1021	ACTGACTTAGATTTATATTGTACAAGAATAGTAACGTTCCCTATGTCCTCGGTATTTAC	1080
QY	1127	TCCTGCTTGAGCGGCAATACGTCGGCTGTATGTACTCAAAAGACCGAAGCGGCACCTTACT	1186
Db	1081	TCCTGCTTGAGCGGCAATACATCGGCCTGTATGTACTCAAAAGACCGAAGCGGCACCTTACT	1140
QY	1187	ACACCATACATGACTATCAAGGTTCAAGTCATCGCCAACTGCAAGATGCAACATGTAGA	1246
Db	1141	ACACCATATATGACTATCAAGGCTCAGTCATCGCTAACTGCAAGATGCAACATGTAGA	1200
QY	1247	TGTGTAAACCCCGGGTATCATATCGCAAAACTATGGGAAGCCGTGTCTCTAATAGAT	1306
Db	1201	TGTGTAAACCCCGGGTATCATATCGCAAAACTATGGGAAGCCGTGTCTCTAATAGAT	1260
QY	1307	AAACAATCATGCAATGTTTATCCTTAGCGGGGATAACTTTAAGGCTCAGTGGGGAATTC	1366
Db	1261	AAACAATCATGCAATGTTTATCCTTAGCGGGGATAACTTTAAGGCTCAGTGGGGAATTC	1320
QY	1367	GATGTAACTTATCAGAGATATCTCAATACAGATTCTCAAGTAATATAACAGGCAAT	1426
Db	1321	GATGTAACTTATCAGAGAAATATCTCAATACAGATTCTCAAGTAATATAACAGGCAAT	1380
QY	1427	CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAG	1486
Db	1381	CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAATAAG	1440
QY	1487	TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCT	1546
Db	1441	TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCT	1500
QY	1547	CTCATTACCTATATCGTTTGTGATCATATCTTGTGTTTGGTATACTTAGCCTGATT	1606
Db	1501	CTCATTACCTATATCGTTTGTGATCATATCTTGTGTTTGGTATACTTAGCCTGATT	1560
QY	1607	CTAGCATGCTACCTAATGTACAAGCAAAAGCGCAACAAAAACCTTATTATGGCTTGGG	1666
Db	1561	CTAGCATGCTACCTAATGTACAAGCAAAAGCGCGCAACAAAGACCTTATTATGGCTTGGG	1620
QY	1667	AATAATATCTAGATCAGATGAGAGGCACCTACAAAAATGTGA	1708
Db	1621	AATAATATCTAGATCAGATGAGAGGCACCTACAAAAATGTGA	1662

Search completed: October 1, 2005, 18:47:36
Job time : 545 secs

QY	61	TTCTACCAAGACCAGCACTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG	120
Db	61		
QY	121	CATCTGTCCGGCAAACTCCATTTGATGGCAGGCTCTTGGCAGCTGCGAGGAATTTGGTTAC	180
Db	121		
QY	181	AGGAGCAAAAGCCGTCAACATATACACCTCATCCGACAGGATCAATCATAGTTAAGCT	240
Db	181		
QY	241	CCTCCGGAATCTGCCAAGGATAAGGAGGATGTGGAAAGCCCTTGGATGCATACAA	300
Db	241		
QY	301	CAGGACATTTGACCACTTTGCTCAACCGCTTGGTGAATTTAGGGCGCCATTTAGGGCGGTG	360
Db	301		
QY	361	TGTGACTACATCTGGAGGGGGAGACAGGGCGCCTTATAGGCGCCATTTAGGGCGGTG	420
Db	361		
QY	421	GGCTCTTTGGGTTGCCAATCTCCGACATAAACAAGGGCGCGAGCTCTGATACAAGCCAA	480
Db	421		
QY	481	ACAAATGCTGCCAAATCTCCGACTTAAAGAGAGATTTGCGCGCAACCAATGAGCGTGT	540
Db	481		
QY	541	GCATGAGTCACTGACGGATTTATCGCACTAGCAGTGGCAGTTGGAGAGATGACAGTT	600
Db	541		
QY	601	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTAGACTGCATCAAAATTCGACAGCA	660
Db	601		
QY	661	AGTTGGTGTAGAGCTCAACTGACCTTAAAGAGAGATTTGCGCGCAACCAATGAGCGTGT	720
Db	661		
QY	721	CACCTCACCTGCTTTAAACAAGCTGACTATTCAGGCACTTTACAATCTAGCTGGTGGAA	780
Db	721		
QY	781	TATGGATTTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	840
Db	781		
QY	841	TAGCGGTTAATCACCGGTAACCTTATTTATACGACTACAGACTCAACTCTTTGGGTAT	900
Db	841		
QY	901	ACAGGTAACCTCACTCAGTCGGGACCTTAATAATATGCTGCGCCACCTACTTGGAAAC	960
Db	901		
QY	961	CTTATCCGTAAGCAACACGAGGATTTGCTCGGCACTTTGCTCCCAAAAGTGTGACACA	1020
Db	961		
QY	1021	GGTGGTTCTGTGATAGAGAACTTGACACCTCATCTGATATAGAACTGACTTAGATTT	1080
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QY	1081	ATATTGTACAGAAATAGTACGTTCCCTATGTCCTGGTATTTATTTCTGCTTTGACGG	1140
Db	1081		
QY	1141	CAATAGCTCGGCCTGTATGTAATCAAGACCGAAGCGCACTTTACTACACATACATGAC	1200
Db	1141		

Db	1141	CAATAGCTCGGCCTGTATGTAATCAAGACCGAAGCGCACTTTACTACACATACATGAC	1200
QY	1201	TATCAAAAGTTTCAGTTCATCGCCNACTGCAAGATGACAAATGATGATGTTAAACCCCC	1260
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QY	1261	GGGTATCATATCGCAAAACTATGGGAAGCGGTCTCTAAATAGATAAAACAATCATGCA	1320
Db	1261		
QY	1321	TGTTTTATCTTTAGCGGGATTAATTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA	1380
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QY	1381	GAAGATATCTCAATACAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
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QY	1441	TGAGCTTTGGGAATGTCAACAACTCGATCAGTAATGCTTTTGAATAAGTTAGAGGAAGCA	1500
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QY	1501	CAGAAAATAGACAAAGTCAATGTCAAACTGACTAGCACATCTGCTCATTTACCTATAT	1560
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QY	1561	CGTTTTGACTATCATATCTCTTTGTTTTGGTATAGCTAGCTGATTTAGCATGTACCT	1620
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QY	1621	AATGTACAAAGCAAGCGCAACAAAACCTTTATTTATGCTTTGGGAATAATCTCTAGA	1680
Db	1621		
QY	1681	TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740
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QY	1801	TGTAGATGACCAAGACGATATACGGGTAGAACCGGTAGAGAGGCGCCCTCAATTGC	1860
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QY	1861	GAGCCAGGCTTCAACACCTCCGTTCTACCGCTTCACCGACAACAGTCTCAATCATGGAC	1920
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QY	2041	TCCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTTGTAGGCAATCCGACTAGG	2100
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Db	2161		
QY	2221	ATTATGAACGCAATAACATCTCTCTTATCAGATTAATGAGAGCTGCAACCAACAGTGGG	2280
Db	2221		

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Db 2221 ATTATGAACGAATAACATCTCTCTTATCAGATTAAATGAGCTGCAAAACAGTGGG 2280
Qy 2281 TGGGGGACACTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAAGAACTCATTTGTA 2340
Db 2281 TGGGGGACACTATCCATGACCCAGATTATATAGGGGGATAGGCAAGAAGAACTCATTTGTA 2340
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Qy 2461 ACCATTACTGCTACACCCCAATATGTAATATGTCGTGATGACAGATCACTCACATTC 2520
Db 2461 ACCATTACTGCTACACCCCAATATGTAATATGTCGTGATGACAGATCACTCACATTC 2520
Qy 2521 TATCAGTATTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGGTATCTTTTCT 2580
Db 2521 TATCAGTATTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGGTATCTTTTCT 2580
Qy 2581 ACTCTGGTTCCATCAACCTGGACGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
Db 2581 ACTCTGGTTCCATCAACCTGGACGACACCCAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
Qy 2641 ACTCCCCGGGTGTGATATGCTGTGTCGAAAGTCAAGGAGACAGAGGAAGATAT 2700
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Qy 2701 AACTCAGCTGTCCCTACCGGATGGTATCATGGGAGGTTAGGTTGCGACGGCCAGTACC 2760
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Qy 2761 GAAAGGACCTAGATGTCACAACTTATTCGGGACTGGGTGCGCAACTCCAGGAGTA 2820
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RESULT 2

US-09-741-744A-134
; Sequence 134, Application US/09741744A
; Publication No. US20030087417A1

; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus

; APPLICANT: de Leeuw, Olav

; APPLICANT: Klaus, Guus

; APPLICANT: Arnoud, Gielkens

; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnosti

; FILE REFERENCE: 2183-4646US

; CURRENT APPLICATION NUMBER: US/09/741,744A

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: PCT/NL99/00377

; PRIOR FILING DATE: 1999-06-17

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 134

; TYPE: DNA

; LENGTH: 15186

; ORGANISM: Newcastle disease virus LaSota

US-09-741-744A-134

Query Match 99.9%; Score 3353.2; DB 10; Length 15186;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGTAGAGATCTCGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 60

Db 4498 ACGGTAGAGATCTCGATCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 4557

Qy 61 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCGCTGGCACTGAGTTG 120

Db 4558 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCGCTGGCACTGAGTTG 4617

Qy 121 CATCTGTCGGCAAACTCCATTTGATGGCAGCCCTTTGACGCTGACAGAAATTTGGTTAC 180

Db 4618 CATCTGTCGGCAAACTCCATTTGATGGCAGCCCTTTGACGCTGACAGAAATTTGGTTAC 4677

Qy 181 AGAGACAAAGCCGTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240

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Qy 241 CCTCCCGAATCTGCCAAGGATAAGAGGATGTGCGAAAGCCCTTTGGATGCATACAA 300

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Qy 301 CAGGACATTGACCACTTTGCTACCCCTTTGGTGACTCTATCCGTAGGATACAAAGTCT 360

Db 4798 CAGGACATTGACCACTTTGCTACCCCTTTGGTGACTCTATCCGTAGGATACAAAGTCT 4857

Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGCGCTTATAGGCGCCATTTGGCGGTGT 420

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Qy 541 GCATGAGGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGGAAGATGCGAGCTT 600

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Db	5158	AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTGACTACAGTATTGGACACCAAAAT	5217		1801	TGTFAGATGACCAAAAGGACGATATACGGGTAGAACCGTAAAGAGAGGCGGCCCTCAATTGC	1860	
QY	721	CACCTCACCTGCTTTAAACAAAGCTGACTATTAGGCACTTTACAATCTAGCTGCTGGAAA	780		6298	TGTAGATGACCAAAAGGACGATATACGGGTAGAACCGTAAAGAGAGGCGGCCCTCAATTGC	6357	
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QY	781	TATGGATTACTTATTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	840		6358	GAGCCAGGCTTCAACAACCTCCGTTCTACCGTTTACCGAACACAGTCTCAATCATGGAC	6417	
Db	5278	TATGGATTACTTATTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG	5337		1921	CGCGCGTTAGCCAAAGTTCCGTTTGTAGAAATGATGAAAGAGAGGCAAAAATATCATGGCGC	1980	
QY	841	TAGCGGCTTAATCACCGGTAAACCTATTCTTATACGACTCACAGACTCAACTCTTGGGTAT	900		6418	CGCGCGTTAGCCAAAGTTTGGTTGTAGAAATGATGAAAGAGAGGCAAAAATATCATGGCGC	6477	
Db	5338	TAGCGGCTTAATCACCGGTAAACCTATTCTTATACGACTCACAGACTCAACTCTTGGGTAT	5397		1981	TTGATATTCCGGATTGCAATCTTATTCTTAAACAGTAGTGACCTTGCTGTATCTGTAGCC	2040	
QY	901	ACAGGTTAACTCTACCTTCAGTCGGGAACCTTAATAATATATGCGTGCCACCTACTTGAAC	960		6478	TTGATATTCCGGATTGCAATCTTATTCTTAAACAGTAGTGACCTTGCTGTATCTGTAGCC	6537	
Db	5398	ACAGGTTAACTCTACCTTCAGTCGGGAACCTTAATAATATATGCGTGCCACCTACTTGAAC	5457		2041	TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCGACTAGG	2100	
QY	961	CTTATCCGTAAGCACCAACAGGGGATTTGCTCGGCACCTTGTCCTCAAAAAGTGTGACACA	1020		6538	TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCGACTAGG	6597	
Db	5458	CTTATCCGTAAGCACCAACAGGGGATTTGCTCGGCACCTTGTCCTCAAAAAGTGTGACACA	5517		2101	ATTTCAGGGCGAAGAAAAGATTACATCTACACTTTGGTTCCATCAAGATGTAGTAGAT	2160	
QY	1021	GGTCGGTTCGTGATAGAGAACTTGACACCTCATCTGTATATAGAAAAGTACTAGATT	1080		6598	ATTTCAGGGCGAAGAAAAGATTACATCTACACTTTGGTTCCATCAAGATGTAGTAGAT	6657	
Db	5518	GGTCGGTTCGTGATAGAGAACTTGACACCTCATCTGTATATAGAAAAGTACTAGATT	5577		2161	AGGATATATAACCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTTGAGACCACA	2220	
QY	1081	ATATTGTACAAGATAGTAACGTTCCCTATGTCCCTGGTATTATTCTGCTTGAAGCG	1140		6658	AGGATATATAACCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATACTTGAGACCACA	6717	
Db	5578	ATATTGTACAAGATAGTAACGTTCCCTATGTCCCTGGTATTATTCTGCTTGAAGCG	5637		2221	ATTATGAAACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGGG	2280	
QY	1141	CAATAGTCGGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACCATATGAC	1200		6718	ATTATGAAACGCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAACACAGTGGG	6777	
Db	5638	CAATAGTCGGCTGTATGTACTCAAGACCGAAGCGCACTTACTACACCATATGAC	5697		2281	TGGGGGCGACCTTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	2340	
QY	1201	TATCAAAGTTTCAGTCATCGCCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCCC	1260		6778	TGGGGGCGACCTTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA	6837	
Db	5698	TATCAAAGTTTCAGTCATCGCCAACTGCAAGATGACAACTGTAGATGTGTAAACCCCCC	5757		2341	GATGATGCTAGTGTCTACATCATCTCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	2400	
QY	1261	GGGTATCATATCGCAAAATATATGGAGAGCGGTGTCTTAATAGATAAACAATCATGCAA	1320		6838	GATGATGCTAGTGTCTACATCATCTCTATCCCTCTGCAATTTCAAGAAACATCTGAATTTT	6897	
Db	5758	GGGTATCATATCGCAAAATATATGGAGAGCGGTGTCTCTAATAGATAAACAATCATGCAA	5817		2401	ATCCCGCGCCTACTACAGGATCAGGTTGCACCTCGAATACCCCTCATTTTGACATGAGTCT	2460	
QY	1321	TGTTTTATCCTTAGCGGGGATACTTTTAAGGCTCAGTGGGGAAATTCGATGTAACCTTATCA	1380		6898	ATCCCGCGCCTACTACAGGATCAGGTTGCACCTCGAATACCCCTCATTTTGACATGAGTCT	6957	
Db	5818	TGTTTTATCCTTAGCGGGGATACTTTTAAGGCTCAGTGGGGAAATTCGATGTAACCTTATCA	5877		2461	ACCATTAATCTGCTACACCCATATGTAATTTGTCTGGATGACAGATCACTCACAATCA	2520	
QY	1381	GAAGAATATCTCAATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440		6958	ACCATTAATCTGCTACACCCATATGTAATTTGTCTGGATGACAGATCACTCACAATCA	7017	
Db	5878	GAAGAATATCTCAATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	5937		2521	TATCAGTATTTAGCACTTGGTGTCTCCGACATCTGCAACAGGGAGGGTATTCTTTTCT	2580	
QY	1441	TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAAATAAGTTAGAGAAAGCAA	1500		7018	TATCAGTATTTAGCACTTGGTGTCTCCGACATCTGCAACAGGGAGGGTATTCTTTTCT	7077	
Db	5938	TGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTGAAATAAGTTAGAGAAAGCAA	5997		2581	ACTCTCCGTTTCCATCAACCTGGACACACCCAAAATCGGAAGTCTTTCAGTGTGAGTGCA	2640	
QY	1501	CAGAAACTAGACAAAGTCAATGTCAAACTGATAGCACATCTGCTCATTAACCTATAT	1560		7078	ACTCTCCGTTTCCATCAACCTGGACACACCCAAAATCGGAAGTCTTTCAGTGTGAGTGCA	7137	
Db	5998	CAGAAACTAGACAAAGTCAATGTCAAACTGATAGCACATCTGCTCATTAACCTATAT	6057		2641	ACTCCCTCCGTTTGTGATATGCTGCTCGAAAGTCAAGGACACAGAGGAAGAAGATTAT	2700	
QY	1561	CGTTTTGACTATCATATCTCTGTTTTTGTGTATCTTAGCCCTGATCTAGCATGCTACCT	1620		7138	ACTCCCTCCGTTTGTGATATGCTGCTCGAAAGTCAAGGACACAGAGGAAGAAGATTAT	7197	
Db	6058	CGTTTTGACTATCATATCTCTGTTTTTGTGTATCTTAGCCCTGATCTAGCATGCTACCT	6117		2701	AACTCAGCTGCTCCCTACGCGGATGTTACATGGAGGTAGGGTTCCACCGCCAGTACCAC	2760	
QY	1621	AATGTACAAGCAAAAGCGCAACAAAACCTTATTATGCTTGGGAATAATATCTCTAGA	1680		7198	AACTCAGCTGCTCCCTACGCGGATGTTACATGGAGGTAGGGTTCCACCGCCAGTACCAC	7257	
Db	6118	AATGTACAAGCAAAAGCGCAACAAAACCTTATTATGCTTGGGAATAATATCTCTAGA	6177		2761	GAAAAGGACCTAGATGCTCAACATTTATTCGGGGAAGTGGGTGCCCAACTACCCAGGAGTA	2820	
QY	1681	TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	1740		7258	GAAAAGGACCTAGATGCTCAACATTTATTCGGGGAAGTGGGTGCCCAACTACCCAGGAGTA	7317	
Db	6178	TCAGATGAGAGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTAATAG	6237		2821	GGGGTGGATCTTTTATTTGACAGCCCGTATGGTTCTCAGTCTACGGAGGGTTAAACCC	2880	
QY	1741	TAATTTTGTGTGAAGTTCTCGTAGTCTGTCAAGTTTCAGAGAGTTTAAGAAAAAATACCGGT	1800					

Db 7318 GGGGGTGGATCTTTTATTGACAGCGCGTATGTTCTCAGTCTACGGAGGTTTAAACCC 7377
Qy 2881 AATTCACCCAGTGACACTGTACAGAAAGGAAATATGTGATATACAAAGCGATACAAATGAC 2940
Db 7378 AATTCACCCAGTGACACTGTACAGAAAGGAAATATGTGATATACAAAGCGATACAAATGAC 7437
Qy 2941 ACATGCCCAGATGACCAAGACTTACCAGATTCGAATGGCCAAAGTCTTCGTATTAAGCCTGGA 3000
Db 7438 ACATGCCCAGATGACCAAGACTTACCAGATTCGAATGGCCAAAGTCTTCGTATTAAGCCTGGA 7497
Qy 3001 CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTTGTCAACATCTTTA 3060
Db 7498 CGGTTTGGTGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTTGTCAACATCTTTA 7557
Qy 3061 GCGGAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 3120
Db 7558 GCGGAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 7617
Qy 3121 AGAATCTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 3180
Db 7618 AGAATCTCACAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATCTTCT 7677
Qy 3181 CCCGGTTTATATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTTCATAGTCTTTAT 3240
Db 7678 CCCGGTTTATATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTTCATAGTCTTTAT 7737
Qy 3241 ACATTCAATGCTTCACTCGGCCAGGTAGTATTCCTTCCAGGCTTCAGCAAGATGCC 3300
Db 7738 ACATTCAATGCTTCACTCGGCCAGGTAGTATTCCTTCCAGGCTTCAGCAAGATGCC 7797
Qy 3301 AACTCGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTATAGAAACC 3358
Db 7798 AACTCGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTATAGAAACC 7855

RESULT 3

US-10-377-718-3
; Sequence 3, Application US/10377718
; Publication No. US20030175291A1
; GENERAL INFORMATION:
; APPLICANT: KUO, Tsun Yuang
; TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO
; FILE REFERENCE: 39734-186920
; CURRENT APPLICATION NUMBER: US/10/377,718
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus (NDV)
US-10-377-718-3

Query Match 99.9%; Score 3353.2; DB 16; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTAGAAGATTCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Db 4498 ACGGGTAGAAGATTCTGGATCCGGTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557
Qy 61 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTCGGCTGGCACTGAGTTG 120
Db 4558 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTCGGCTGGCACTGAGTTG 4617
Qy 121 CATCTGCCGCAAACTCCTATGATGATGAGCGCTCTTGACGCTCAGGAATTTGGTTAC 180
Db 4618 CATCTGCCGCAAACTCCTATGATGATGAGCGCTCTTGACGCTCAGGAATTTGGTTAC 4677
Qy 181 AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240
Db 4678 AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 4737

Qy 241 CCTCCGAATCTGCCCAAGGATAAGGAGCATGTGCGAAAGCCCCCTTGGATGCATACAA 300
Db 4738 CCTCCGAATCTGCCCAAGGATAAGGAGCATGTGCGAAAGCCCCCTTGGATGCATACAA 4797
Qy 301 CAGGACATTGACCACTTTTGTCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAAGATC 360
Db 4798 CAGGACATTGACCACTTTTGTCTCACCCCTTTGGTGACTCTATCCGTAGGATACAAAGATC 4857
Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGGGCGCTTATAGGCGGCATATTTGGCGGTGT 420
Db 4858 TGTGACTACATCTGGAGGGGGAGACAGGGGGCGCTTATAGGCGGCATATTTGGCGGTGT 4917
Qy 421 GGCTCTTGGGGTTCGAACCTGCCGACAAATAAAGAGAGCAATTTGCCGCAACCAATGAGGCTGT 540
Db 4918 GGCTCTTGGGGTTCGAACCTGCCGACAAATAAAGAGAGCAATTTGCCGCAACCAATGAGGCTGT 4977
Qy 481 ACAAATTCGCTCCCAACATCTCCGACTTAAAGAGAGCAATTTGCCGCAACCAATGAGGCTGT 540
Db 4978 ACAAATTCGCTCCCAACATCTCCGACTTAAAGAGAGCAATTTGCCGCAACCAATGAGGCTGT 5037
Qy 541 GCATGAGGTCACTGACCGGATTTATCGCAACTAGCAGTGGCAGTTGGGAGATGCAAGCAGTT 600
Db 5038 GCATGAGGTCACTGACCGGATTTATCGCAACTAGCAGTGGCAGTTGGGAGATGCAAGCAGTT 5097
Qy 601 TGTTAATGACCAATTTTAAACAGCTCAGGANTTAGCATCAAAATTTGACACAGCA 660
Db 5098 TGTTAATGACCAATTTTAAACAGCTCAGGANTTAGCATCAAAATTTGACACAGCA 5157
Qy 661 AGTTGGTGTAGAGCTCAACCTGTACCTTAAACGAAATTCAGTACAGTATTCGGACCAAAAT 720
Db 5158 AGTTGGTGTAGAGCTCAACCTGTACCTTAAACGAAATTCAGTACAGTATTCGGACCAAAAT 5217
Qy 721 CACTTCACTGCTTTTAAACAGCTGACTATTTACGGCACTTTTACAAATTAGCTGGTGGAAA 780
Db 5218 CACTTCACTGCTTTTAAACAGCTGACTATTTACGGCACTTTTACAAATTAGCTGGTGGAAA 5277
Qy 781 TATGGATTACTTATTTAGTAAGTTAGGTGATAGGAAACAATCAACTCAGCTCATTAATCGG 840
Db 5278 TATGGATTACTTATTTAGTAAGTTAGGTGATAGGAAACAATCAACTCAGCTCATTAATCGG 5337
Qy 841 TAGCGGCTTAATCACCGGTAAACCTTCTTATACGACTCACAGACTCAACTCTTTGGGTAT 900
Db 5338 TAGCGGCTTAATCACCGGTAAACCTTCTTATACGACTCACAGACTCAACTCTTTGGGTAT 5397
Qy 901 ACAGGTAACCTCTACCTTCAGTTCGGGAACCTTAAATAATATATGCGTGCCCACTTCTGGAAC 960
Db 5398 ACAGGTAACCTCTACCTTCAGTTCGGGAACCTTAAATAATATATGCGTGCCCACTTCTGGAAC 5457
Qy 961 CTTATCCGTAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGTGACACA 1020
Db 5458 CTTATCCGTAAGCAACACAGGGGATTTGGCTCGGCACTTTGTCCCAAAAGTGTGACACA 5517
Qy 1021 GGTGCGTTCGTGATAGAAGAACTTGACACTCATCTGATATAGAACTGACTTAGATTT 1080
Db 5518 GGTGCGTTCGTGATAGAAGAACTTGACACTCATCTGATATAGAACTGACTTAGATTT 5577
Qy 1081 ATATTGTACAAAGATAGTAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG 1140
Db 5578 ATATTGTACAAAGATAGTAACGTTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG 5637
Qy 1141 CAATACTCGGCTGTATGATCTCAAAAGACGGAAGCGCACTTACTACACATACATGAC 1200
Db 5638 CAATACTCGGCTGTATGATCTCAAAAGACGGAAGCGCACTTACTACACATACATGAC 5697
Qy 1201 TATCAAGGTTGACTCATCGCAACTTCGAAGATGACAACTAGATGTGTAAACCCCC 1260
Db 5698 TATCAAGGTTGACTCATCGCAACTTCGAAGATGACAACTAGATGTGTAAACCCCC 5757
Qy 1261 GGGTATCATATCGCAAACTTATGGAGAACCGGTGTCTCTAATAGATAAAACAATCATGCAA 1320
Db 5758 GGGTATCATATCGCAAACTTATGGAGAACCGGTGTCTCTAATAGATAAAACAATCATGCAA 5817
Qy 1321 TGTTTTATCCTTAGGCGGGATAAATTTAAGGCTCAGTGGGGAAATTCGATGTAACCTTATCA 1380

[illegible]

RESULT 4

RESOL 4
US-10-429-735-3

; Sequence 3, Application US/10429735

; Publication No. US20030207836A1

GENERAL INFORMATION:

APPLICANT: KUO, Tsun Yuang

; TITLE OF INVENTION: VACCINE ACC

; TITLE OF INVENTION: IN POULTRY

FILE REFERENCE: 39734-18849

; CURRENT APPLICATION NUMBER: US/10/429,735

Db 6478 |||||TTGATA||TCGGGATGCAATCTTATCTTAAACAGTAGTACCCTTGGCTATATCTGTAGCC 6537
Qy 2041 TCCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTGTAGGCATACCGACTAGG 2100
Db 6538 TCCCTTTTATATAGCATGGGGCTAGCACACCTTAGCGATCTTGTAGGCATACCGACTAGG 6597
Qy 2101 ATTTCCAGGGCAGAAAGAAATACATCTACACTCTGGTCCCAATCAAGATGTAGTAGAT 2160
Db 6598 ATTTCCAGGGCAGAAAGAAATACATCTACACTCTGGTCCCAATCAAGATGTAGTAGAT 6657
Qy 2161 AGGATATATAGCAAGTGGCCCTTAGCTCTCCGTTGGCATGTGTAATACTAGAGACACA 2220
Db 6658 AGGATATATAGCAAGTGGCCCTTAGCTCTCCGTTGGCATGTGTAATACTAGAGACACA 6717
Qy 2221 ATTTAGAACCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGGG 2280
Db 6718 ATTTAGAACCAATAACATCTCTCTTATCAGATTAATGGAGCTGCAAAACACAGTGGG 6777
Qy 2281 TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 6778 TGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 6837
Qy 2341 GATGATCTAGTATGATCAATCATTTCTATCCCTCTGCATTTCAAGAACATCTGAATTTT 2400
Db 6838 GATGATCTAGTATGATCAATCATTTCTATCCCTCTGCATTTCAAGAACATCTGAATTTT 6897
Qy 2401 ATCCCGGGCCTACTACAGATCAGGTTGCACCTCGAATACCTCATTTGACATGAGTCT 2460
Db 6898 ATCCCGGGCCTACTACAGATCAGGTTGCACCTCGAATACCTCATTTGACATGAGTCT 6957
Qy 2461 ACCATTACTGCTACACCCATAATGTAATTTGCTGGATGTCAGAGATCACTCACATTCA 2520
Db 6958 ACCATTACTGCTACACCCATAATGTAATTTGCTGGATGTCAGAGATCACTCACATTCA 7017
Qy 2521 TATCAGTATTTAGCAGTTGGTGTCTCCGACATCTGCAACAGGGAGGGTATTTCTTTCT 2580
Db 7018 TATCAGTATTTAGCAGTTGGTGTCTCCGACATCTGCAACAGGGAGGGTATTTCTTTCT 7077
Qy 2581 ACTCTGGGTTCCATCAACCTGGAGCACACCCAAATCGGAAGTCTGCAGTGTAGTGCA 2640
Db 7078 ACTCTGGGTTCCATCAACCTGGAGCACACCCAAATCGGAAGTCTTGCAGTGTAGTGCA 7137
Qy 2641 ACTCCCCTGGTGTGATATGCTGTGCTCGAAAGTCAAGAGTACAGAGAGGAAGATTAT 2700
Db 7138 ACTCCCCTGGTGTGATATGCTGTGCTCGAAGTCAAGAGTACAGAGAGGAAGATTAT 7197
Qy 2701 AACTCAGCTGTCCCTACGCGGATGGTACATGGGAGGTTAGGGTTCGACGGCCAGTACCAC 2760
Db 7198 AACTCAGCTGTCCCTACGCGGATGGTACATGGGAGGTTAGGGTTCGACGGCCAGTACCAC 7257
Qy 2761 GAAAAGGACCTAGATGTCAACAATTTATTCGGGACCTGGGTGGCCAACTACCCAGGATG 2820
Db 7258 GAAAAGGACCTAGATGTCAACAATTTATTCGGGACCTGGGTGGCCAACTACCCAGGATG 7317
Qy 2821 GGGGTGGATCTTTTATTTGACGCGGATGTTCTCAGTCTACGAGGAGTTAAACCC 2880
Db 7318 GGGGTGGATCTTTTATTTGACGCGGATGTTCTCAGTCTACGAGGAGTTAAACCC 7377
Qy 2881 AATTACCCCACTGACTGTACAGGAAGGAAATATGTGATATACAAGCGATACAATGAC 2940
Db 7378 AATTACCCCACTGACTGTACAGGAAGGAAATATGTGATATACAAGCGATACAATGAC 7437
Qy 2941 ACATGCCAGATGAGCAAGACTACAGATTCGAATGGCCAACTTCGTATAGCCCTGGA 3000
Db 7438 ACATGCCAGATGAGCAAGACTACAGATTCGAATGGCCAACTTCGTATAGCCCTGGA 7497
Qy 3001 CGGTTTGTGGGAAACGCATACACAGCGCTATCTTATCTATCAAGGTGTCAACATCCTTA 3060
Db 7498 CGGTTTGTGGGAAACGCATACACAGCGCTATCTTATCTATCAAGGTGTCAACATCCTTA 7557
Qy 3061 GGGGAAGACCCGGTATCTGACTGTATCCGCCCAACACAGTCACTCATGTGGGGCGGAAGGC 3120

Db 7558 GSCGAAGACCCGGTACTGACTGTACCGCCCAACACAGTCACTCAATGGGGCGGAAGGC 7617
Qy 3121 AGAATTTCTCACAGTAGGGACATCTCATTTTCTTGTATCAACAGAGGTCACTCATACTTCTCT 3180
Db 7618 AGAATTTCTCACAGTAGGGACATCTCATTTTCTTGTATCAACAGAGGTCACTCATACTTCTCT 7677
Qy 3181 CCGCGTATTATATATCTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTTAT 3240
Db 7678 CCGCGTATTATATATCTATGACAGTCAGCAACAAACAGCCACTCTTCATAGTCTTTAT 7737
Qy 3241 ACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC 3300
Db 7738 ACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTGTACTCGAGTCTATACAGATCCATATCCCTATCTTCTATAGAAACC 7855

RESULT 5
US-10-824-782-134
; Sequence 134, Application US/10824782
; Publication No. US20040234552A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus; de Leeuw, Olav; Klaus, Guus; Gielkens, Arnold
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/10/824,782
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/788,232
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus strain LaSota
US-10-824-782-134

Query Match 99.9%; Score 3353.2; DB 20; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGGGTAGAGATTCTGGATCCCGGTTGGCCCTCCAGGTGCAAGATGGGCTCCAGACC 60
Db 4498 ACGGGTAGAAGATTCTGGATCCCGGTTGGCCCTCCAGGTGCAAGATGGGCTCCAGACC 4557
Qy 61 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGCGCTGGCACTGAGTTG 120
Db 4558 TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTGCGCTGGTACTGAGTTG 4617
Qy 121 CATCTGTCCGGCAAACTCCATTGATGCGCAGGCTCTTTCAGCTGTCAGGAAATGTGTGTTAC 180
Db 4618 CATCTGTCCGGCAAACTCCATTGATGCGCAGGCTCTTTCAGCTGTCAGGAAATGTGTGTTAC 4677
Qy 181 AGAGACAAGACCGCTCAACATATACACCTATCCAGACAGGATCAATCATAGTTAAGCT 240
Db 4678 AGAGACAAGACCGCTCAACATATACACCTATCCAGACAGGATCAATCATAGTTAAGCT 4737
Qy 241 CTTCCCGAATCTCCCAAGGATTAAGAGGATGTGCGAAAGCCCTTGGATGCATACAA 300
Db 4738 CTTCCCGAATCTCCCAAGGATTAAGAGGATGTGCGAAAGCCCTTGGATGCATACAA 4797
Qy 301 CAGGACATTGACCACTTTTGTCTACCCCCCTTGGTGACTCTATCCGTAGGATACAAGATC 360
Db 4798 CAGGACATTGACCACTTTTGTCTACCCCCCTTGGTGACTCTATCCGTAGGATACAAGATC 4857
Qy 361 TGTGACTACATCTGGAGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATTCGCCGTGT 420
Db 4858 TGTGACTACATCTGGAGGGGGAGACAGGGGCGCTTATAGGCGCCATTTATTCGCCGTGT 4917

QY 421 GCCTCTTGGGGTTGCAACTGCCGCAAAATACACAGCGCGCGAGCTCTGTATCAAGCCAA 480
Db 4918 GGCCTTTGGGGTTGCAACTGCCGCAAAATACACAGCGCGCGAGCTCTGTATCAAGCCAA 4977
QY 481 ACAAAATGCTGCAACATCTCTCCGACTTTAAAGAGAGCAATTCGCGCAACCAATAGGCGTGT 540
Db 4978 ACAAAATGCTGCAACATCTCTCCGACTTTAAAGAGAGCAATTCGCGCAACCAATAGGCGTGT 5037
QY 541 GCATGAGTCTACTGACGGAATATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT 600
Db 5038 GCATGAGTCTACTGACGGAATATCGCAACTAGCAGTGGCAGTTGGGAAGATGCAAGCAGTT 5097
QY 601 TGTAAATGACCAATTTAATAAAGCTCAGGAATTTAGACTGCAATTAAGCTGCAATTAAGCTGCA 660
Db 5098 TGTAAATGACCAATTTAATAAAGCTCAGGAATTTAGACTGCAATTAAGCTGCAATTAAGCTGCA 5157
QY 661 AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTTGACTACAGTATTCGAGCACAAT 720
Db 5158 AGTTGGTGTAGAGCTCAACCTGTACTTAACCGAATTTGACTACAGTATTCGAGCACAAT 5217
QY 721 CACTTCACCTGCTTTAAACAAGCTGACTTATTCAGGCACTTTTCAATCTAGCTGTGGGAAA 780
Db 5218 CACTTCACCTGCTTTAAACAAGCTGACTTATTCAGGCACTTTTCAATCTAGCTGTGGGAAA 5277
QY 781 TATGGAATTAATTTAGCTTAAGTATAGGTTAGGGAACAATCAACTCAGCTCATTTAATCGG 840
Db 5278 TATGGAATTAATTTAGCTTAAGTATAGGTTAGGGAACAATCAACTCAGCTCATTTAATCGG 5337
QY 841 TAGCGGCTTAATCACCGGTAAACCTTATTCATACGACTCACAGACTCAACTCTTGGGTAT 900
Db 5338 TAGCGGCTTAATCACCGGTAAACCTTATTCATACGACTCACAGACTCAACTCTTGGGTAT 5397
QY 901 ACAGTAACTCTACCTTCAGTGGGAACCTTAAATAATATGGTGCGCACTACTTTGGAAAC 960
Db 5398 ACAGTAACTCTACCTTCAGTGGGAACCTTAAATAATATGGTGCGCACTACTTTGGAAAC 5457
QY 961 CTTATTCGCTAAGCAACAACAGGGGATTTGCCCTCGGCACTTGTCCCAAAAGTGTGACACA 1020
Db 5458 CTTATTCGCTAAGCAACAACAGGGGATTTGCCCTCGGCACTTGTCCCAAAAGTGTGACACA 5517
QY 1021 GGTGGTCTGTGATAGAGAACTTGACACCTCATACGTATAGAGAACTGACTTAGATTT 1080
Db 5518 GGTGGTCTGTGATAGAGAACTTGACACCTCATACGTATAGAGAACTGACTTAGATTT 5577
QY 1081 ATATTGTACAGAAATAGTAAAGTTCCTTATGTCCCTGGTATTTATTCCTGCTGAGCGG 1140
Db 5578 ATATTGTACAGAAATAGTAAAGTTCCTTATGTCCCTGGTATTTATTCCTGCTGAGCGG 5637
QY 1141 CAATACGTGGGCTGTATGTACTCAAGACCGAAGCGGCACTTACTACCAATATGAC 1200
Db 5638 CAATACGTGGGCTGTATGTACTCAAGACCGAAGCGGCACTTACTACCAATATGAC 5697
QY 1201 TATCAAGGTTTCAGTCATCGGCACTGCAAGATGACACATGTAGTGTAAACCCCCC 1260
Db 5698 TATCAAGGTTTCAGTCATCGGCACTGCAAGATGACACATGTAGTGTAAACCCCCC 5757
QY 1261 GGGTATCATATCGCAAAATATGGAAGAGCGGTGTCTCTAATAGATAAACAATCATGCAA 1320
Db 5758 GGGTATCATATCGCAAAATATGGAAGAGCGGTGTCTCTAATAGATAAACAATCATGCAA 5817
QY 1321 TGTTTTATCTTATAGCGGGATAAATTTTAAAGGCTCAGTGGGAAATTCGATGTAACTTATCA 1380
Db 5818 TGTTTTATCTTATAGCGGGATAAATTTTAAAGGCTCAGTGGGAAATTCGATGTAACTTATCA 5877
QY 1381 GAAGATATCTCAATACAGATTTCTCAAGTAAATATATACAGCAATCTTGTATCTCAAC 1440
Db 5878 GAAGATATCTCAATACAGATTTCTCAAGTAAATATATACAGCAATCTTGTATCTCAAC 5937
QY 1441 TGAGCTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTTGAATAGTTAGAGGAAGCAA 1500
Db 5938 TGAGCTTGGGAATGTCAACAACCTCGATCAGTAAATGCTTTTGAATAGTTAGAGGAAGCAA 5997
QY 1501 CAGAAAACCTAGACAAAGTCAATGTGTCAAACCTGACTAGCACATCTGCTCTCATTAACCTATPAT 1560

Db 5998 CAGAAAACCTAGACAAAGTCAATGTCAAACCTGACTAGCACATCTGCTCTCATTAACCTATPAT 6057
QY 1561 CGTTTGGACTATCATATCTCTTGTGTTTGGTATATCTTAGCCTGATTTCTAGCATGTACCT 1620
Db 6058 CGTTTGGACTATCATATCTCTTGTGTTTGGTATATCTTAGCCTGATTTCTAGCATGTACCT 6117
QY 1621 AATGTACAGCAAAAGGGGCAACAAAAAACCCTTATTTATGGCTTGGGAATAATATCTCTAGA 1680
Db 6118 AATGTACAGCAAAAGGGGCAACAAAAAACCCTTATTTATGGCTTGGGAATAATATCTCTAGA 6177
QY 1681 TCAGATGAGGAGGCACTCAAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTTAATAG 1740
Db 6178 TCAGATGAGGAGGCACTCAAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTTAATAG 6237
QY 1741 TAAATTTGTGTGAAGTTCTGCTAGTCTGTCTAGTTCAGAGGTTTAAAGAAAAAATACCCGT 1800
Db 6238 TAAATTTGTGTGAAGTTCTGCTAGTCTGTCTAGTTCAGAGGTTTAAAGAAAAAATACCCGT 6297
QY 1801 TGTAGATGACCAAAAGGAGCATATACGGGTAGAAACGGTAAAGAGAGCGCCCTCTCAATTGC 1860
Db 6298 TGTAGATGACCAAAAGGAGCATATACGGGTAGAAACGGTAAAGAGAGCGCCCTCTCAATTGC 6357
QY 1861 GAGCCAGGCTTCACAACTCCGTTCTACCGCTTCCACGACAAACAGTCTCAATCATGAC 1920
Db 6358 GAGCCAGGCTTCACAACTCCGTTCTACCGCTTCCACGACAAACAGTCTCAATCATGAC 6417
QY 1921 CGCCCGCTTACCCAAAGTTGCGTTAGAGAAATGATGAAAGAGAGGCAAAAAATACATGGCG 1980
Db 6418 CGCCCGCTTACCCAAAGTTGCGTTAGAGAAATGATGAAAGAGAGGCAAAAAATACATGGCG 6477
QY 1981 TTGATATTCGCGATGCGAATCTTATTTTAAACAGTGTAGTGTGGCTTATATCTGTAGCC 2040
Db 6478 TTGATATTCGCGATGCGAATCTTATTTTAAACAGTGTAGTGTGGCTTATATCTGTAGCC 6537
QY 2041 TCCCTTTTATATAGCATGGGGCTTAGCACACTAGCATCTTGTAGGCATACCGACTAGG 2100
Db 6538 TCCCTTTTATATAGCATGGGGCTTAGCACACTAGCATCTTGTAGGCATACCGACTAGG 6597
QY 2101 ATTTTCAGGGCAGAGAAAGATTAATCTACACTTGGTTCCAATCAAGATGTAGTAGAT 2160
Db 6598 ATTTTCAGGGCAGAGAAAGATTAATCTACACTTGGTTCCAATCAAGATGTAGTAGAT 6657
QY 2161 AGGATATATAAGCAAGTGGCGCTTGTAGTCTCCGTTGGCATTTGTTAAATATCTGAGACACA 2220
Db 6658 AGGATATATAAGCAAGTGGCGCTTGTAGTCTCCGTTGGCATTTGTTAAATATCTGAGACACA 6717
QY 2221 ATTTAGAACGCAATTAATCTCTCTTATCAGATTAATGAGCTGCAAAACAGTGGG 2280
Db 6718 ATTTAGAACGCAATTAATCTCTCTTATCAGATTAATGAGCTGCAAAACAGTGGG 6777
QY 2281 TGGGGGGCACCCTATCCATGACCCAGATTTATATAGGGGGGATAGGCAAAAGAACTCATTTGTA 2340
Db 6778 TGGGGGGCACCCTATCCATGACCCAGATTTATATAGGGGGGATAGGCAAAAGAACTCATTTGTA 6837
QY 2341 GATGATCTAGTGTGATGATCATCATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 2400
Db 6838 GATGATCTAGTGTGATGATGATCATCATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 6897
QY 2401 ATCCCGGGCCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTTGAATGAGTGTCT 2460
Db 6898 ATCCCGGGCCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTTGAATGAGTGTCT 6957
QY 2461 ACCCATTTACTGCTACACCCCAATATGTAATTTGTCTGATGATGATGATGATGATGATGATGAT 2520
Db 6958 ACCCATTTACTGCTACACCCCAATATGTAATTTGTCTGATGATGATGATGATGATGATGAT 7017
QY 2521 TATCAGTATTTAGCACTTGGTGTCTCGGACATCTGCAACAGGGAGGGTATTTCTTTCT 2580
Db 7018 TATCAGTATTTAGCACTTGGTGTCTCGGACATCTGCAACAGGGAGGGTATTTCTTTCT 7077
QY 2581 ACTCTGGCTTCATCACTCGGACGACACCCCAAAATCGGAAGTCTTGCAGTGTGAGTGCA 2640

Db	7078	ACTCTGCGTTCCATCAACCTGGACGACACCCAAATCGGAAGTCTTGGCAGTGTGAGTGCA	7137
Qy	2641	ACTCCCCCTGGGTGTGTGATATGCTGTGCTCGAAAGTACACGAGACAGAGGAAGAAGATTAT	2700
Db	7138	ACTCCCCCTGGGTGTGTGATATGCTGTGCTCGAAAGTACACGAGACAGAGGAAGAAGATTAT	7197
Qy	2701	AATCTAGCTGTCCCTACCGCGATGGTATACATGGGAGGTTAGGGTTTCGACGGCCAGTACCAC	2760
Db	7198	AATCTAGCTGTCCCTACCGCGATGGTATACATGGGAGGTTAGGGTTTCGACGGCCAGTACCAC	7257
Qy	2761	GAAGAAGACCTAGATGTCAACAATTTATTCGGGACATGGGTGGCCAACTACCCAGAGTA	2820
Db	7258	GAAGAAGACCTAGATGTCAACAATTTATTCGGGACCTGGGTGGCCAACTACCCAGAGTA	7317
Qy	2821	GGGGGTGGATCTTTATTTGACAGCCGGTATGTTCTCAGTCTACGAGGGTTTAAACCC	2880
Db	7318	GGGGGTGGATCTTTATTTGACAGCCGGTATGTTCTCAGTCTACGAGGGTTTAAACCC	7377
Qy	2881	AATTCACCCAGTGCACCTGTACAGGAAGGGAATATGTGATATACAAGCGATACAATGAC	2940
Db	7378	AATTCACCCAGTGCACCTGTACAGGAAGGGAATATGTGATATACAAGCGATACAATGAC	7437
Qy	2941	ACATGCCAGATGAGGAAGTACACAGATTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA	3000
Db	7438	ACATGCCAGATGAGGAAGTACACAGATTCGAATGGCCAAAGTCTTCGTATAGCCCTGGA	7497
Qy	3001	CGGTTTGGTGGGAAACSCATACAGCAGCGCTATCTTATCTCAAGGTGTCAACATCCTTA	3060
Db	7498	CGGTTTGGTGGGAAACSCATACAGCAGCGCTATCTTATCTCAAGGTGTCAACATCCTTA	7557
Qy	3061	GGCGAAGACCCGGTACTGTACGCGCCCAACACAGTCACTCATGTGGGGCGGCGAAGGC	3120
Db	7558	GGCGAAGACCCGGTACTGTACGCGCCCAACACAGTCACTCATGTGGGGCGGCGAAGGC	7617
Qy	3121	AGAAATTCACAGTAGGGAATCTCATTTCTGTGTATCAACAGAGGTCACTCATCTCTCT	3180
Db	7618	AGAAATTCACAGTAGGGAATCTCATTTCTGTGTATCAACAGAGGTCACTCATCTCTCT	7677
Qy	3181	CCGCGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTCATAGTCTCTAT	3240
Db	7678	CCGCGTTATTATATCTTATGACAGTCAAGCAACAAACAGCCACTCTTCATAGTCTCTAT	7737
Qy	3241	ACATTCAAATGCCITTCACCTCGCCAGGTAGTATCCCTTTCGAGGCTTCAGCAAGATGCCCC	3300
Db	7738	ACATTCAAATGCCITTCACCTCGCCAGGTAGTATCCCTTTCGAGGCTTCAGCAAGATGCCCC	7797
Qy	3301	AATCTGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	3358
Db	7798	AATCTGTGTGTACTGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC	7855

RESULT 6
US-10-788-232-134
; Sequence 134, Application US/10788232
; Publication No. US20040235134A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernardus; de Leeuw, Olav; Klaus, Guus; Gielkens, Arnold
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnostic
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/10/788,232
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus strain LaSota
US-10-788-232-134

Query Match 99.9%; Score 3353.2; DB 20; Length 15186;
Best Local Similarity 99.9%; Pred. No. 0;

		Matches 3355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	1	ACGGGTAGAGAGATCTTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	60
Db	4498	ACGGGTAGAGAGATCTTGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACC	4557
Qy	61	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTCGCTGGCACTGAGTTG	120
Db	4558	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGGTTCGCTGGCACTGAGTTG	4617
Qy	121	CATCTGTCCGGCAAACTCCATTTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGGCTTAC	180
Db	4618	CATCTGTCCGGCAAACTCCATTTGATGGCAGGCTCTTTCAGCTGCGAGGAATTTGGCTTAC	4677
Qy	181	AGGAGACAAAGCGCTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	240
Db	4678	AGGAGACAAAGCGCTCAACATATACACCTCATCCAGACAGGATCAATCATAGTTAAGCT	4737
Qy	241	CCTCCCGAATCTGCCCAAGGATAAGGAGCATGTGCGAAAGCCCTTTCGATGCATACAA	300
Db	4738	CCTCCCGAATCTGCCCAAGGATAAGGAGCATGTGCGAAAGCCCTTTCGATGCATACAA	4797
Qy	301	CAGGACATTTGACCACTTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAAAGTTC	360
Db	4798	CAGGACATTTGACCACTTTGCTCACCCCTTGGTGAATCTATCCGTAGGATACAAAGTTC	4857
Qy	361	TGTGACTTACATCTGGAGGGGGAGACAGGGGCGCTTATAGGGCCCATTTATTTGGCGGTGT	420
Db	4858	TGTGACTTACATCTGGAGGGGGAGACAGGGGCGCTTATAGGGCCCATTTATTTGGCGGTGT	4917
Qy	421	GGCTCTTGGGTTGCAACTGCCGCACAAAATAACAGCGCGCGCAGTCTCTGATACAAAGC	480
Db	4918	GGCTCTTGGGTTGCAACTGCCGCACAAAATAACAGCGCGCGCAGTCTCTGATACAAAGC	4977
Qy	481	ACAAATGTCCCAACATCTCCGACTTAAAGAGACATTTCCGCAACCAATGAGGCTGT	540
Db	4978	ACAAATGTCCCAACATCTCCGACTTAAAGAGACATTTCCGCAACCAATGAGGCTGT	5037
Qy	541	GCATGAGTCACTACGCGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	600
Db	5038	GCATGAGTCACTACGCGGATTTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT	5097
Qy	601	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGATGTCATCAAAATTCGACAGCA	660
Db	5098	TGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGATGTCATCAAAATTCGACAGCA	5157
Qy	661	AGTTGTTGATAGCTCAACCTGTACCTAACCGAATTTGATACAGTATTCGACACCAAT	720
Db	5158	AGTTGTTGATAGCTCAACCTGTACCTAACCGAATTTGATACAGTATTCGACACCAAT	5217
Qy	721	CACCTTCACCTGCTTTAAACAAAGCTGACTTTTACAGGCATTTTCAATCTAGCTGGTGA	780
Db	5218	CACCTTCACCTGCTTTTAAACAAAGCTGACTTTTACAGGCATTTTCAATCTAGCTGGTGA	5277
Qy	781	TATGATTACTTATTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCAATTAATCGG	840
Db	5278	TATGATTACTTATTGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCAATTAATCGG	5337
Qy	841	TAGCGGCTTAATCACCGGTAAACCTTATCTATACGACTCACAGACTCAACTCTTGGGTAT	900
Db	5338	TAGCGGCTTAATCACCGGTAAACCTTATCTATACGACTCACAGACTCAACTCTTGGGTAT	5397
Qy	901	ACAGGTAACTCTACCTTTTCAGTCGGGAACCTTAAATAATATGCGTGGCCACCTACTTGA	960
Db	5398	ACAGGTAACTCTACCTTTTCAGTCGGGAACCTTAAATAATATGCGTGGCCACCTACTTGA	5457
Qy	961	CTTATCCGTAAAGCAACACCGGGATTTGCCTCGGCACTTGTCCCAAAAGTGTGTACACA	1020
Db	5458	CTTATCCGTAAAGCAACACCGGGATTTGCCTCGGCACTTGTCCCAAAAGTGTGTACACA	5517
Qy	1021	GGTCCGTTCTGTGATAGAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATTT	1080
Db	5518	GGTCCGTTCTGTGATAGAGAACTTGACACCTCATCTGTATAGAACTGACTTAGATTT	5577

Qy	1081	ATATTGTACAAAGATAGTAAGTTCCTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	1140
Db	5578	ATATTGTACAAAGATAGTAAGTTCCTCCCTATGTCCCTGGTATTTATTCCTGCTTGAGCGG	5637
Qy	1141	CAATACGTCGGCCTGTATGTACTCAAGACCGAAGCGCAGCTTACTACACCATACATGAC	1200
Db	5638	CAATACGTCGGCCTGTATGTACTCAAGACCGAAGCGCAGCTTACTACACCATACATGAC	5697
Qy	1201	TATCAAAAGTTTCAGTCATCGCCAACTGCAAGATGACAAATGTAGATGTGTAACCCGCC	1260
Db	5698	TATCAAAAGTTTCAGTCATCGCCAACTGCAAGATGACAAATGTAGATGTGTAACCCGCC	5757
Qy	1261	GGGTATCATATCGCAAAACTATGAGAACCGGTGTCTCTATATAGATAAACAATCATGCAA	1320
Db	5758	GGGTATCATATCGCAAAACTATGAGAACCGGTGTCTCTATATAGATAAACAATCATGCAA	5817
Qy	1321	TGTTTTATCCTTAGCGGGATAACTTTTAAAGCTCAGTGGGAAATTCGATGTAACTTTATCA	1380
Db	5818	TGTTTTATCCTTAGCGGGATAACTTTTAAAGCTCAGTGGGAAATTCGATGTAACTTTATCA	5877
Qy	1381	GAAGAATATCTCAATACAAAGATTCCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	1440
Db	5878	GAAGAATATCTCAATACAAAGATTCCTCAAGTAATAATAACAGGCAATCTTGATATCTCAAC	5937
Qy	1441	TGAGCTTGGGAATGTCAACAACTCGATCAGTAAATGTCTTTGAAATAGTTAGAGGAAGCAA	1500
Db	5938	TGAGCTTGGGAATGTCAACAACTCGATCAGTAAATGTCTTTGAAATAGTTAGAGGAAGCAA	5997
Qy	1501	CAGAAACTAGCAAAAGTCAATGTCAAACTCAGCTAGCAGCATCTCTCTCATTTACTATAT	1560
Db	5998	CAGAAACTAGCAAAAGTCAATGTCAAACTCAGCTAGCAGCATCTCTCTCATTTACTATAT	6057
Qy	1561	CGTTTGGACTATCATATCTCTTTGTTTGGTATATCTTAGCCCTGATTTAGCATGCTACCT	1620
Db	6058	CGTTTGGACTATCATATCTCTTTGTTTGGTATATCTTAGCCCTGATTTAGCATGCTACCT	6117
Qy	1621	AATGTACAAGCAAAAGGCGCAACAAAACTTATATGTTGGTTGGGAATAATATCTTAGA	1680
Db	6118	AATGTACAAGCAAAAGGCGCAACAAAACTTATATGTTGGTTGGGAATAATATCTTAGA	6177
Qy	1681	TCAGATGAGGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATAG	1740
Db	6178	TCAGATGAGGCCACTACAAAATGTGAACACAGATGAGGAACGAAGTTTCCCTTAATAG	6237
Qy	1741	TAAATTGTGTGAAAGTTCTCGTAGTCTCTCAGTTTCAGAGAGTTAAGAAAAAATACCGGT	1800
Db	6238	TAAATTGTGTGAAAGTTCTCGTAGTCTCTCAGTTTCAGAGAGTTAAGAAAAAATACCGGT	6297
Qy	1801	TGTAGATGACCAAAAGGACGATATACGGGTAGAACGGTGAAGAGGCGCCCTCAATTGC	1860
Db	6298	TGTAGATGACCAAAAGGACGATATACGGGTAGAACGGTGAAGAGGCGCCCTCAATTGC	6357
Qy	1861	GAGCAGGCTTCACAACTCGCTTCTACCGCTTCAACGACAAAGTCTCTCAATCATGGAC	1920
Db	6358	GAGCAGGCTTCACAACTCGCTTCTACCGCTTCAACGACAAAGTCTCTCAATCATGGAC	6417
Qy	1921	CGCGCGTTAGCCAAAGTTGCGTTAGAGAAATCGATGAAAGAGGCAAAAAATACATGCGC	1980
Db	6418	CGCGCGTTAGCCAAAGTTGCGTTAGAGAAATCGATGAAAGAGGCAAAAAATACATGCGC	6477
Qy	1981	TTGATATTTCCGGATTGCAATCTTATTTTAAACAGTAGTGACCTTGGCTATATCTGTAGCC	2040
Db	6478	TTGATATTTCCGGATTGCAATCTTATTTTAAACAGTAGTGACCTTGGCTATATCTGTAGCC	6537
Qy	2041	TCCCTTTTATATAGATGGGGCTTAGCACCTAGCGATCTTTGAGGCATACCGACTAGG	2100
Db	6538	TCCCTTTTATATAGATGGGGCTTAGCACCTAGCGATCTTTGAGGCATACCGACTAGG	6597
Qy	2101	ATTTCCAGGCGAGAAAGATTAATCTACCTTGGTTCCCAATCAAGATGTAGTAGAT	2160
Db	6598	ATTTCCAGGCGAGAAAGATTAATCTACCTTGGTTCCCAATCAAGATGTAGTAGAT	6657

Qy	2161	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATFACTGAGACACA	2220
Db	6658	AGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCATTTGTTAAATFACTGAGACACA	6717
Qy	2221	ATTATGAACCAATAAATCAATCTCTCTTATCAGATTAATGGAGCTGCAAAACAAGTGGG	2280
Db	6718	ATTATGAACCAATAAATCAATCTCTCTTATCAGATTAATGGAGCTGCAAAACAAGTGGG	6777
Qy	2281	TGGGGGGACCTATTCATAGCCAGATTAATATAGGGGGGATAGGCAAAAGAATCATTTGTA	2340
Db	6778	TGGGGGGACCTATTCATAGCCAGATTAATATAGGGGGGATAGGCAAAAGAATCATTTGTA	6837
Qy	2341	GATCATGCTAGTGATGATCAGATCAATCTATCCCTCTGCAATTTCAAGAACATCTGAAATTT	2400
Db	6838	GATCATGCTAGTGATGATCAGATCAATCTATCCCTCTGCAATTTCAAGAACATCTGAAATTT	6897
Qy	2401	ATCCCGGGCCCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTTGAATGAGTGCT	2460
Db	6898	ATCCCGGGCCCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTTGAATGAGTGCT	6957
Qy	2461	ACCATTTACTGCTACACCCATAATGTAATATGTTGCTGGATGCGAGATCACTCAATTC	2520
Db	6958	ACCATTTACTGCTACACCCATAATGTAATATGTTGCTGGATGCGAGATCACTCAATTC	7017
Qy	2521	TATCAGTATTTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGTTATCTTTCT	2580
Db	7018	TATCAGTATTTAGCACTTGGTGTCTCGGACATCTGCAACAGGAGGTTATCTTTCT	7077
Qy	2581	ACTCTGGGTTCCATCAACCTGGAGCAGACCCCAAAATCGGAAGTCTTGCAAGTGTGAGTGCA	2640
Db	7078	ACTCTGGGTTCCATCAACCTGGAGCAGACCCCAAAATCGGAAGTCTTGCAAGTGTGAGTGCA	7137
Qy	2641	ACTCCCTGGGTTGTGATATGCTGTCTCGAAAGTCAACGAGACAGAGGAAGAAGATTAT	2700
Db	7138	ACTCCCTGGGTTGTGATATGCTGTCTCGAAAGTCAACGAGACAGAGGAAGAAGATTAT	7197
Qy	2701	AACCTCAGTGTCCCTACGCGGATGGTACATGGGAGTTAGGTTTCGAGCGCCAGTACCAC	2760
Db	7198	AACCTCAGTGTCCCTACGCGGATGGTACATGGGAGTTAGGTTTCGAGCGCCAGTACCAC	7257
Qy	2761	GAAAGGACCTAGATGTCAACAATTTATCGGGGACTGGGTGGCCAACTACCCAGGAGTA	2820
Db	7258	GAAAGGACCTAGATGTCAACAATTTATCGGGGACTGGGTGGCCAACTACCCAGGAGTA	7317
Qy	2821	GGGGTGGATCTTTTATTTGAACGCGGTATGTTCTCAGTCTACGAGGGTTAAAAACC	2880
Db	7318	GGGGTGGATCTTTTATTTGAACGCGGTATGTTCTCAGTCTACGAGGGTTAAAAACC	7377
Qy	2881	AATTCACCCAGTGACACTGTACAGGAAGGAAATATGTGATATACAGCGATACAAATGAC	2940
Db	7378	AATTCACCCAGTGACACTGTACAGGAAGGAAATATGTGATATACAGCGATACAAATGAC	7437
Qy	2941	ACATGCCAGATGAGCAAGACTACAGATTCGAATGCCAAGTCTTCGTATAAGCCTTGA	3000
Db	7438	ACATGCCAGATGAGCAAGACTACAGATTCGAATGCCAAGTCTTCGTATAAGCCTTGA	7497
Qy	3001	CGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTT	3060
Db	7498	CGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTT	7557
Qy	3061	GGCGAAGACCGGTACTGTACTGTAACCGCCCAACACAGTCACTCATGCGGGGCGAAGGC	3120
Db	7558	GGCGAAGACCGGTACTGTACTGTAACCGCCCAACACAGTCACTCATGCGGGGCGAAGGC	7617
Qy	3121	AGATTTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCTATCATCTCTCT	3180
Db	7618	AGATTTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCTATCATCTCTCTCT	7677
Qy	3181	CCCCGGTTTATATATCTTATGACAGTCAAGCAAAAAACAGCCACTCTTTCTAGTCTTTAT	3240
Db	7678	CCCCGGTTTATATATCTTATGACAGTCAAGCAAAAAACAGCCACTCTTTCTAGTCTTTAT	7737
Qy	3241	ACATTCATGCTTCTACTCGGCCAGGTAGTATCCCTTTGCCAGGCTTCAGCAAGATGCCCC	3300

Db	7738	ACATTCATGCTTCTACTCGGCCAGGTAGTATCCCTTGCCAGGCTTCAGCAAGATGCCCC	7797
Qy	3301	AATCGGTGTGTACTCGAGTCTATACAGATCCATATCCCCCTAACTCTTATAGAAACC	3358
Db	7798	AATCGGTGTGTACTCGAGTCTATACAGATCCATATCCCCCTAACTCTTATAGAAACC	7855
RESULT 7			
US-10-440-419-55			
: Sequence 55, Application US/10440419			
: Publication No. US20030224017A1			
: GENERAL INFORMATION:			
: APPLICANT: SAMAL, SIBA K.			
: APPLICANT: HUANG, ZHUHUI			
: TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS			
: TITLE OF INVENTION: VACCINES OR VACCINE VECTORS			
: FILE REFERENCE: 108172-00096			
: CURRENT APPLICATION NUMBER: US/10/440,419			
: CURRENT FILING DATE: 2003-05-19			
: PRIOR APPLICATION NUMBER: 09/926,431			
: PRIOR FILING DATE: 2002-03-06			
: PRIOR APPLICATION NUMBER: PCT/US00/06700			
: PRIOR FILING DATE: 2000-05-05			
: PRIOR APPLICATION NUMBER: 60/381,462			
: PRIOR FILING DATE: 2002-05-17			
: PRIOR APPLICATION NUMBER: 60/171,072			
: PRIOR FILING DATE: 1999-12-16			
: PRIOR APPLICATION NUMBER: 60/132,597			
: PRIOR FILING DATE: 1999-05-05			
: NUMBER OF SEQ ID NOS: 56			
: SOFTWARE: PatentIn Ver. 2.1			
: SEQ ID NO 55			
: LENGTH: 15900			
: TYPE: DNA			
: ORGANISM: Artificial Sequence			
: FEATURE:			
: OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for			
US-10-440-419-55			
Query Match 99.7%; Score 3346.8; DB 17; Length 15900;			
Best Local Similarity 99.8%; Pred. No. 0;			
Matches 3351; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
Qy	1	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC	60
Db	5212	ACGGGTAGAAGATTCTGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC	5271
Qy	61	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCGCTGGCAGTGTG	120
Db	5272	TTCTACCAAGAACCCAGCACCTATGATGCTGACTATCCGGTTGCGCTGGTACTGAGTTG	5331
Qy	121	CATCTGTCCGGCAACTCCATTGATGGAGGCGCTTTGCGAGCTGCAGGAATTTGGTTAC	180
Db	5332	CATCTGTCCGGCAACTCCATTGATGGAGGCGCTTTGCGAGCTGCAGGAATTTGGTTAC	5391
Qy	181	AGGAGACAAAGCCGCTCAACATATACACCTCATCCCGACAGGATCAATCATGTTAAGCT	240
Db	5392	AGGAGACAAAGCCGCTCAACATATACACCTCATCCCGACAGGATCAATCATGTTAAGCT	5451
Qy	241	CCTCCCGAATCTGCCAAGGATAGGAGGCGATGTGCGAAAGCCCTTGGATGCATACAA	300
Db	5452	CCTCCCGAATCTGCCAAGGATAGGAGGCGATGTGCGAAAGCCCTTGGATGCATACAA	5511
Qy	301	CAGGACATTGACCACTTTGCTCAACCCCTTTGGTGACTCTATCCGTTAGGATACAAGATC	360
Db	5512	CAGGACATTGACCACTTTGCTCAACCCCTTTGGTGACTCTATCCGTTAGGATACAAGATC	5571
Qy	361	TGTGACTACATCTGGAGGGGGACAGGGGCGCTTATAGGCGCCATTATTCGCGGTGT	420
Db	5572	TGTGACTACATCTGGAGGGGGGACAGGGGCGCTTATAGGCGCCATTATTCGCGGTGT	5631
Qy	421	GGCTCTTTGGGGTTGCAACTGCGCGCACAAATACAGCGCGCGCAGCTCTGTATACAAGCAA	480

Db 6712 CAGAAACTAGACAAAGTCAATGTCAAACTGACACGACATCTGCTCTCATTAACCTATAT 6771
Qy 1561 CGTTTTGACATACATATCTCTGTTTTTGGTATATCTAGCCCTGATCTAGCATGCTACCT 1620
Db 6772 CGTTTTGACATACATATCTCTGTTTTTGGTATATCTAGCCCTGATCTAGCATGCTACCT 6831
Qy 1621 AATGTACAGCAAAAGCGGCAACAAAACCTTATATGCTTGGGATATATCTCTAGA 1680
Db 6832 AATGTACAGCAAAAGCGGCAACAAAACCTTATATGCTTGGGATATATCTCTAGA 6891
Qy 1681 TCAGATGAGGCCACTACAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAG 1740
Db 6892 TCAGATGAGGCCACTACAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTAATAG 6951
Qy 1741 TAAATTTGTGAAAGTTCTGCTAGTCTGTCTAGTTTCAGAGTTAAGAAAAAATACCGGT 1800
Db 6952 TAAATTTGTGAAAGTTCTGCTAGTCTGTCTAGTTTCAGAGTTAAGAAAAAATACCGGT 7011
Qy 1801 TGTAGATGACCAAGGACGATATACGGGTAGAAACGTTAAGAGAGCGCCCTCAATTGC 1860
Db 7012 TGTAGATGACCAAGGACGATATACGGGTAGAAACGTTAAGAGAGCGCCCTCAATTGC 7071
Qy 1861 GAGCAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAACAGTCTCAATCATGAC 1920
Db 7072 GAGCAGGCTTCACAACTCCGTTCTACCGCTTCACCGACAAACAGTCTCAATCATGAC 7131
Qy 1921 CGCCCGTTAGCCAAAGTTGCTTAGAAGATGATGAAGAGAGGCAAAAAATACATGGCG 1980
Db 7132 CGCCCGTTAGCCAAAGTTGCTTAGAAGATGATGAAGAGAGGCAAAAAATACATGGCG 7191
Qy 1981 TTGATATCCGGATTGCAATCTTATTTAAACAGTAGTACCTTGGCTTATATCTGTAGCC 2040
Db 7192 TTGATATCCGGATTGCAATCTTATTTAAACAGTAGTACCTTGGCTTATATCTGTAGCC 7251
Qy 2041 TCCCTTTTATATAGCATGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG 2100
Db 7252 TCCCTTTTATATAGCATGGGGCTAGCACACTAGCGATCTTGTAGGCATACCGACTAGG 7311
Qy 2101 ATTTCCAGGGCAGAAAGAAATACATCTACACTTGGTTCCAAATCAAGATGTAGTAGAT 2160
Db 7312 ATTTCCAGGGCAGAAAGAAATACATCTACACTTGGTTCCAAATCAAGATGTAGTAGAT 7371
Qy 2161 AGATATATAGCAAGTGGCCCTGAGTCTCCGTTGGCATTTGTTAAATACGTAGACACCA 2220
Db 7372 AGATATATAGCAAGTGGCCCTGAGTCTCCGTTGGCATTTGTTAAATACGTAGACACCA 7431
Qy 2221 ATTATGACGCAATAACATCTCTCTTATCAGATTTAATGAGCTGCAAAACAGTGGG 2280
Db 7432 ATTATGACGCAATAACATCTCTCTTATCAGATTTAATGAGCTGCAAAACAGTGGG 7491
Qy 2281 TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Db 7492 TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 7551
Qy 2341 GATGATGCTAGTAGTACATCATATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 2400
Db 7552 GATGATGCTAGTAGTACATCATATTTCTATCCCTCTGCAATTTCAAGAACATCTGAATTTT 7611
Qy 2401 ATCCCGGGCTACTACAGGATCAGGTTGCACTCGAATACCTCATTTTGACATGAGTCT 2460
Db 7612 ATCCCGGGCTACTACAGGATCAGGTTGCACTCGAATACCTCATTTTGACATGAGTCT 7671
Qy 2461 ACCATTACTGCTACACCCATAAATGTAATTTGCTGATGACAGATCACTACATTTCA 2520
Db 7672 ACCATTACTGCTACACCCATAAATGTAATTTGCTGATGACAGATCACTACATTTCA 7731
Qy 2521 TATCAGTATTTAGCATTTGGTGTCTCCGACATCTGCAACAGAGGGATTTCTTTTCT 2580
Db 7732 TATCAGTATTTAGCATTTGGTGTCTCCGACATCTGCAACAGAGGGATTTCTTTTCT 7791
Qy 2581 ACTCTGGTTCCATCAACCTGGACACACCCAAAATCGGAAGTCTTCAGTGTGAGTGCA 2640
Db 7792 ACTCTGGTTCCATCAACCTGGACACACCCAAAATCGGAAGTCTTCAGTGTGAGTGCA 7851

Qy 2641 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGAGACAGAGGAAGATATAT 2700
Db 7852 ACTCCCTGGGTTGTGATATGCTGTGCTCGAAAGTCAAGAGACAGAGGAAGATATAT 7911
Qy 2701 AACTCAGCTGTCCCTACGCGATGCTACATGGGAGGTTAGGTTTCGACGGCCAGTACCAC 2760
Db 7912 AACTCAGCTGTCCCTACGCGATGCTACATGGGAGGTTAGGTTTCGACGGCCAGTACCAC 2791
Qy 2761 GAAAAGGACCTAGATGTCAACAATATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 2820
Db 7972 GAAAAGGACCTAGATGTCAACAATATTTCGGGACCTGGGTGGCCAACTACCCAGGAGTA 8031
Qy 2821 GGGGTTGATCTTTTATTGACAGCCGCTATGTTCTCAGTCTACGAGGGTTTAAACCC 2880
Db 8032 GGGGTTGATCTTTTATTGACAGCCGCTATGTTCTCAGTCTACGAGGGTTTAAACCC 8091
Qy 2881 AATTTCACCCAGTACACTGTACAGGAAGGAAATATGTATATACAGCGATACATGAC 2940
Db 8092 AATTTCACCCAGTACACTGTACAGGAAGGAAATATGTATATACAGCGATACATGAC 8151
Qy 2941 ACATGCCAGATGAGCAAGACTACAGATTTCGAATGSCCAAGTCTTCGTATAAGCCTGGA 3000
Db 8152 ACATGCCAGATGAGCAAGACTACAGATTTCGAATGSCCAAGTCTTCGTATAAGCCTGGA 8211
Qy 3001 CGGTTTGGTGGGAAAACGATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTCTTA 3060
Db 8212 CGGTTTGGTGGGAAAACGATACAGCAGGCTATCTTATCTATCAAGGTGTCAACATCTCTTA 8271
Qy 3061 GGGAGACCCGGTACTGACTGTACCGCCCAACACACTCACCTCATGCGGGCCGGAAGGC 3120
Db 8272 GGGAGACCCGGTACTGACTGTACCGCCCAACACACTCACCTCATGCGGGCCGGAAGGC 8331
Qy 3121 AGAATTCACAGTAGGAGCATCTCATTTCTGTATCAAGAGGCTCATCATCTTCTCT 3180
Db 8332 AGAATTCACAGTAGGAGCATCTCATTTCTGTATCAAGAGGCTCATCATCTTCTCT 8391
Qy 3181 CCGCGTTATTATATCTTATCTATGACAGTCAAGCAACAAAACAGCCTCTTCATAGTCTTAT 3240
Db 8392 CCGCGTTATTATATCTTATCTATGACAGTCAAGCAACAAAACAGCCTCTTCATAGTCTTAT 8451
Qy 3241 ACATTCAATGCCCTCACTCGCCAGGAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC 3300
Db 8452 ACATTCAATGCCCTCACTCGCCAGGAGTATCCCTTGCAGGCTTCAGCAAGATGCCCC 8511
Qy 3301 AACTCGTGTCTACTGAGTCTATACAGATCCCATATCCCTAACTCTTATAGAAACC 3358
Db 8512 AACTCGTGTCTACTGAGTCTATACAGATCCCATATCCCTAACTCTTATAGAAACC 8569

RESULT 8

US-10-440-419-56
; Sequence 56, Application US/10440419
; Publication No. US20030224017A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, ZHUHUI
; APPLICANT: SAMAL, SIBA K.
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS
; FILE OF INVENTION: 108172-00096
; CURRENT APPLICATION NUMBER: US/10/440,419
; PRIOR FILING DATE: 2003-05-19
; PRIOR FILING DATE: 09/926,431
; PRIOR FILING DATE: 2002-03-06
; PRIOR FILING DATE: PCT/US00/06700
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/381,462
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/171,072
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/132,597
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 15882
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV
US-10-440-419-56

Query Match 95.28; Score 3198; DB 17; Length 15882;
Best Local Similarity 97.08; Pred. No. 0;
Matches 3258; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 ACGGTAGAGATTCTTGATCCCGTTGGCGCCCTCCAGGTGCAAGATGGCTCCAGACC 60
DB 4498 ACGGTAGAGATTCTTGATCCCGTTGGCGCCCTCTAGGTGCAAGATGGGCCAGACC 4557

QY 61 TTCTACCAAGAACCCAGCACTATGATGTGACTATCCGGTTGCGCTGGCACTGAGTTG 120
DB 4558 TTCTACCAAGAACCCAGTACTATGATGTGACTGTCCGAGTCCGCTGCTACTGAGTTG 4617

QY 121 CATCTGTCGGCAAACTCCATTGATGTCAGCGCTCTTGGCAGCTGCGAGGAATTGTTGTTAC 180
DB 4618 CATCTGTCGGCAAACTCCATTGATGTCAGCGCTCTTGGCGCTGCGAGGAATTGTTGTTAC 4677

QY 181 AGGAGACAAAGCCGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 240
DB 4678 AGGAGACAAAGCAGTCAACATATACCTCATCCAGACAGGATCAATCATAGTTAAGCT 4737

QY 241 CCTCCGAATCTGCCAAGGATAGGAGGATGTGCGAAAGCCCCCTTGGATCATACAA 300
DB 4738 CCTCCGAATCTGCCAAGGATAGGAGGATGTGCGAAAGCCCCCTTGGATCATACAA 4797

QY 301 CAGGACATTGACACATTGCTACCCCCCTTGTGACTCTATCCGTAGGATACAGAGTC 360
DB 4798 CAGGACATTGACACATTGCTACCCCCCTTGTGACTCTATCCGTAGGATACAGAGTC 4857

QY 361 TGTGACTTACATCTGGAGGGGGAGACAGGGCGCCTTATAGGCGCCATTATTCGGCGTGT 420
DB 4858 TGTAACTACATCTGGAGGGAGGAGACAGAAACGCTTATAGGCGCCATTATTCGGCGTGT 4917

QY 421 GGCTCTTGGGTTGCAACTCCCGCACAAATTAACAGCGCGCGAGCTCTGTATACAAGCCAA 480
DB 4918 GGCTCTTGGGTTGCAACTCTGCACAAATAACAGCGCGCGAGCTCTGTATACAAGCCAA 4977

QY 481 ACAAATGCTGCCAATCTCCGACTTAAAGAGAGCAATTCGCCCAACCAATCAGGCTGT 540
DB 4978 ACAAATGCTGCCAATCTCCGACTTAAAGAGAGCAATTCGCCCAACCAATCAGGCTGT 5037

QY 541 GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT 600
DB 5038 GCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGGAAGATGACGAGTT 5097

QY 601 TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTAGACTGCATCAAAATTCACAGCA 660
DB 5098 TGTTAATGACCAATTTAATAAAGCAGCTCAGGAATTAGACTGCATCAGAAATTCACAGCA 5157

QY 661 AGTTGGTGTAGAGTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT 720
DB 5158 AGTTGGTGTAGAGTCAACCTGTACCTAACCGAATTGACTACAGTATTCGGACCAAAAT 5217

QY 721 CACTTCACTGCTTAAACAAGCTGACTATTAGGCACTTTTCAATCTAGCTGCTGGAAA 780
DB 5218 CACTTCACTGCTTAAACAAGCTGACTATTAGGCACTTTTCAATCTAGCTGCTGGAAA 5277

QY 781 TATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 840
DB 5278 TATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTCAGCTCATTAATCGG 5337

QY 841 TAGCGGCTTAATCAGCGGTAAACCTTATCTATACGACTACAGACTCAACTCTTGGGTAT 900
DB 5338 TAGCGGCTTAATCAGCGGTAAACCTTATCTGTACGACTACAGACTCAACTCTTGGGTAT 5397

QY 901 ACAGGTAACCTCTACCTTCAGTCGGGAACCTAAATAATATATGCGTGCCACCTACTTGGAAAC 960
DB 5398 ACAGGTAACCTCTACCTTCAGTCGGGAACCTAAATAATATATGCGTGCCACCTACTTGGAAAC 5457

QY 961 CTTATCCGTAAGCACAAACGAGGATTTGCTCGGCACCTTGTCCAAAAGTGTGTGACACA 1020
DB 5458 CTTATCCGTAAGCACAAACGAGGATTTGCTCGGCACCTTGTCCAAAAGTGTGTGACACA 5517

QY 1021 GGTCCGGTCTGTGATAGAGAAGCTTCACACCTCATCTGTATATAGAAAGTGCATGATTT 1080
DB 5518 GGTCCGGTCTGTGATAGAGAAGCTTCACACCTCATCTGTATATAGAAAGTGCATGATTT 5577

QY 1081 ATATTGTACAAGAAATAGTAACGTTCCCTATGTCCCTCGTGTATTTATTCCTGCTTGAGCGG 1140
DB 5578 ATATTGTACAAGAAATAGTAACATTCCTATGTCCCTCGTGTATTTATTCCTGCTTGAGCGG 5637

QY 1141 CAATACGTCCGCTGTATGTACTCAAAAGACCGAAGGCGCACTTACTACACATACATGAC 1200
DB 5638 CAATACGTCCGCTGTATGTACTCAAAAGACCGAAGGCGCACTTACTACGCTACATGAC 5697

QY 1201 TATCAAGGTTTCAGTTCATCGCCAACTGCAAGATGCAACATGTAGATGTGTAAACCCCC 1260
DB 5698 TATCAAGGTTTCAGTTCATCGCTAACTGCAAGATGCAACATGTAGATGTGTAAACCCCC 5757

QY 1261 GGGTATCATATCGCAAAACTATGGAAGCCGCTGTCTCTAAATAGATAAAACAATCATGCAA 1320
DB 5758 GGGTATCATATCGCAAAACTATGGAAGCCGCTGTCTCTAAATAGATAAAACAATCATGCAA 5817

QY 1321 TGTATTATCTTTAGGCGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 1380
DB 5818 TGTATTATCTTTAGGCGGGATAACTTTAAGGCTCAGTGGGGAATTCGATGTAACTTATCA 5877

QY 1381 GAAGATAATCTCAATCAAGATTTCTCAAGTAAATAAAGAGCAATCTTGATATCTCAAC 1440
DB 5878 GAAGATAATCTCAATCAAGATTTCTCAAGTAAATAAAGAGCAATCTTGATATCTCAAC 5937

QY 1441 TGAGCTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTGAATAAGTTAGAGGAAGCAA 1500
DB 5938 TGAGCTTGGGAATGTCAACAACTCGATCAGTAAATGCTTTGAATAAGTTAGAGGAAGCAA 5997

QY 1501 CAGAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGTCTCTCATATCTATAT 1560
DB 5998 CAGAAATAGACAAAGTCAATGTCAAACTGACTAGACATCTGTCTCTCATATCTATAT 6057

QY 1561 CGTTTGTGACTATCATATCTCTTGTGTTTGTGTACTGTAGCTGATCTTACGATGCTACCT 1620
DB 6058 CGTTTGTGACTATCATATCTCTTGTGTTTGTGTACTGTAGCTGATCTTACGATGCTACCT 6117

QY 1621 AATGTACAAAGCAAAAGCGCAACAAAAACCTTATTTATGGCTTGGGAATAATACTCTAGA 1680
DB 6118 AATGTATAGCAAAAGCGCAACAAAAACCTTATTTATGGCTTGGGAATAATACTCTAGA 6177

QY 1681 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCTAATAG 1740
DB 6178 TCAGATGAGAGCCACTACAAAAATGTGAACACAGATGAGGAACGAAGTTTCCTAATAG 6237

QY 1741 TAAATTTGTGTAAGTTCTTGGTAGTCTGTCTGAGTTTACAGAGTTTAAAGAAAACTACCGGT 1800
DB 6238 TAAATTTGTGTAAGTTCTTGGTAGTCTGTCTGAGTTTACAGAGTTTAAAGAAAACTACCGGT 6297

QY 1801 TGTAGATGACCAAGGACGATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTGC 1860
DB 6298 TGTAGATGACCAAGGACGATATACGGGTAGAACCGTAAAGAGAGGCGCCCTCAATTGC 6357

QY 1861 GAGCCAGGCTTCAACCTCCGTTCTACCGCTTACCGCAACACAGTCTCTCAATCATGGAC 1920
DB 6358 GAGCCAGGCTTCAACCTCCGTTCTACCGCTTACCGCAACACAGTCTCTCAATCATGGAC 6417

QY 1921 CGGCGCTTAGCCAAAGTTGGTTAGAAATGATGAAGAGAGGCAAAATATACATCGGC 1980
DB 6418 CGGCGCTTAGCCAAAGTTGGTTAGAAATGATGAAGAGAGGCAAAATATACATCGGC 6477

QY 1981 TTGATATTCCGGATTGCAATCTTTTCTTAAACAGTAGTAGCTTGGCTATATCTGTAGCC 2040

Db 6478 TTGATATTCGGGATTGCAATCTTACTTTAAAGTAGTAGTACCTTAGCTACATCTGTAGCC 6537
Qy TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGATCTTTGTAGGCATACCGACTAGG 2100
Db TCCCTTTTATATAGCATGGGGCTAGCACACCTAGCGACCTTTGTAGGCATACCGACGAG 6597
Qy ATTTCCAGGGCAGAGAAAGATTACATCTACACTTGGTTCCAAATCAAGATGTAGTAGAT 2160
Db ATTTCTAGGGCAGAGAAAGATTACATCTGCACCTTGGTTCCAAATCAAGATGTAGTAGAT 6657
Qy AGGATATATAGCAAGTGGCCCTTGGAGTCCGTTGGCATTTGTTAAATACATGAGACACACA 2220
Db AGGATATATAGCAAGTGGCCCTTGGAGTCCGTTGGCATTTGTTAAATCAATGAGACACACA 6717
Qy ATTTATGAACGCAATAACATCTCTCTCTTATCAGATTAAATGGAGCTGCAAAACAAAGTGGG 2280
Db ATTTATGAACGCAATAACATCTCTCTCTTATCAGATTAAATGGAGCTGCAAAACAAAGTGGG 6777
Qy TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 2340
Db TGGGGGGCACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAGAACTCATTTGTA 6837
Qy GATGATGCTAGTGTGATCATCATCTTCTATCCCTCTGCATTTCAAGACATCTGAATTTT 2400
Db GATGATGCTAGTGTGATCATCATCTTCTATCCCTCTGCATTTCAAGACATCTGAATTTT 6897
Qy ATCCCGGCGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATCAGTGCT 2460
Db ATCCCGGCGCTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATCAGTGCT 6957
Qy ACCCATTAAGTCTACACCCATAATGTAATGTTGCTGATGCGAGATCACTCAACTCA 2520
Db ACCCATTAAGTCTACACCCATAATGTAATGTTGCTGATGCGAGATCACTCAACTCA 7017
Qy TATCAGTATTTAGCATTTGGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTCT 2580
Db TATCAGTATTTAGCATTTGGTGTCTCGGACATCTGCAACAGGAGGATTTCTTTCT 7077
Qy ACTCTGCGTTCATCAGTCTGATGACACCCAAATCGGAAGTCTTGAGTGTGAGTGCA 2640
Db ACTCTGCGTTCATCAGTCTGATGACACCCAAATCGGAAGTCTTGAGTGTGAGTGCA 7137
Qy ACTCCCTGGGTTGTGATATCTGTCTCGAAAGTACGGAGACAGAGAAAGATPAT 2700
Db ACTCCCTGGGTTGTGATATCTGTCTCGAAAGTACGGAGACAGAGAAAGATPAT 7197
Qy AACTCAGCTGTCCCTACCGGATGATGATGAGGTTAGGTTTCGACGGCCAGTACCAC 2760
Db AACTCAGCTGTCCCTACCGGATGATGATGAGGTTAGGTTTCGACGGCCAGTACCAC 7257
Qy GAAAGGACCTAGATGTCACAACTATTTCGGGACTGGGTGGCCAACTACCCAGGAGTA 2820
Db GAAAGGACCTAGATGTCACAACTATTTCGGGACTGGGTGGCCAACTACCCAGGAGTA 7317
Qy GGGGGTGGATCTTTTATTGACAGCGCGGTATGGTTCTCAGTCTACGGAGGTTTAAACCC 2880
Db GGGGGTGGATCTTTTATTGACAGCGCGGTATGGTTCTCAGTCTACGGAGGTTTAAACCC 7377
Qy AATTCAACCCAGTGACACTGTACAGGAGGAAATATGTGATATACAGCGATACATGAC 2940
Db AATTCAACCCAGTGACACTGTACAGGAGGAAATATGTGATATACAGCGATACATGAC 7437
Qy ACATGCCAGATGACAGACTTACCAGATTTCGAATGGCCAACTTCTGATTAAGCCCTGGA 3000
Db ACATGCCAGATGACAGACTTACCAGATTTCGAATGGCCAACTTCTGATTAAGCCCTGGA 7497
Qy CGGTTTGGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGGTTCAACATCTTTA 3060
Db CGGTTTGGTGGGAAACGATACAGAGGCTATCTTATCTATCAAGGTTCAACATCTTTG 7557
Qy GGGGAGACCCGGTATCTGACTACCGCCCAACACAGTCACTCATGGGGGCGGAGGCC 3120

Db 7558 GCGAGAGACCAGTACTGACTGTACCGCCCAACACAGTCACTCATGGGGCCGAAGGC 7617
Qy 3121 AGAATTTCAAGTAGGGACATCTCAATTTCTGTATATCAACGAGGCTCATCATCTTCTCT 3180
Db 7618 AGAATTTCAAGTAGGGACATCTCAATTTCTGTATATCAAGCGAGGCTCATCATCTTCTCT 7677
Qy 3181 CCCGGTTATATATCTCTATGACAGTACAGCAACAAACAGCCACTCTTCATAGTCTTAT 3240
Db 7678 CCCGGTTATATATCTCTATGACAGTACAGCAACAAACAGCCACTCTTCATAGTCTTAT 7737
Qy 3241 ACATTTCAATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 3300
Db 7738 ACATTTCAATGCTTCACTCGGCCAGGTAGTATCCCTTCCAGGCTTCAGCAAGATGCCCC 7797
Qy 3301 AACTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 3358
Db 7798 AACTCGTGTGTACTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGAAACC 7855

RESULT 9
US-09-881-457A-1
; Sequence 1, Application US/09881457A
; Patent No. US20020081316A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: No. US20020081316A1el Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105K1QKQK
; CURRENT APPLICATION NUMBER: US/09/881,457A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3570
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1194)..(2888)
; OTHER INFORMATION: NDV Fusion Protein
; NAME/KEY: misc feature
; LOCATION: (1355)
; OTHER INFORMATION: n = any nucleotide
US-09-881-457A-1

Query Match 50.7%; Score 1701.6; DB 9; Length 3570;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;
Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACTTCTTCAAGAAACC 75
Db 1199 TCGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACTTCTTCAAGAAACC 1258
Qy 76 AGCACCTATGATGCTGACTATCCGGTTGCCCTGGCACTGAGTTGCATCTGTCCGGCAA 135
Db 1259 AGCACCTATGATGCTGACTATCCGGTTGCCCTGGCACTGAGTTGCATCTGTCCGGCAA 1318

136 CTCATTGATGGAGGCTCTTGAGCTGCAGGAATGTGGTTACAGGAGACAAAGCCGT 195
1319 CTCATTGATGGAGGCTCTTGAGCTGCAGG-ACNTGGTTACAGGAGCAAGCAAT 1377
196 CAACATATACACCTCATCCAGACAGGATCAATCATATAGTTAAAGTCTCTCCCGAATCTGCC 255
1378 CAACATATACACCTCATCCAGACAGG-TCAATCATAT-TTAAAGTCTCTCCCGAATCTGCC 1435
256 CAAGGATAGGAGGATGTGCGAAAGCCCTTGGATGCAATCAACAGGACATTTGACCAC 315
1436 AAAGGATAGGAGGATGTGCGAAAGCCCTTGGATGCAATCAACAGGACATTTGACCAC 1495
316 TTTTGCTCACCCCTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 375
1496 TTTTGCTCACCCCTTGGTGACTCTATCCGTAGGATCAAGAGTCTGTGACTACATCTGG 1555
376 AGGGGGAGACAGGGGGCCCTTATAGGCGCCATTTATTTGGCGGTGTGGCTCTTGGGGTTGC 435
1556 AGGGGGAGACAGGGGGCCCTTATAGGCGCCATTTATTTGGCGGTGTGGCTCTTGGGGTTGC 1615
436 AACTGCGGCAAAATTAACAGCGCGCGAGCTCTGTATCAAGCCAAACAAAATGCTGCCAA 495
1616 AACTGCGGCAAAATTAACAGCGCGCGAGCTCTGTATCAAGCCAAACAAAATGCTGCCAA 1675
496 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGGTCACTGA 555
1676 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGGTCACTGA 1735
556 CGGATTATCCCACTAGCAGTGGCAGTTGGGAAGATGACAGCAGTTGTTTAAATGACCAATT 615
1736 CGGATTATCCCACTAGCAGTGGCAGTTGGGAAGATGACAGCAGTTGTTTAAATGACCAATT 1795
616 TAATAAAGAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCAAGTTGGTTAGAGCT 675
1796 TAATAAAGAGCTCAGGAATTAGACTGCATCAAAATTTGCACAGCAAGTTGGTTAGAGCT 1855
676 CAACCTGTACTTAACCGAATTTGACTACAGTATTCGAGCAACAATCACTTCACTGCTTT 735
1856 CAACCTGTACTTAACCGAATTCGACTACAGTATTCGAGCAACAATCACTTCACTGCTTT 1915
736 AAACAAGCTGACTATTACAGCAGCTTTTACAACTAGCTGGTGGAAATATGGATTACTTATT 795
1916 AAACAAGCTGACTATTACAGCAGCTTTTACAACTAGCTGGTGGAAATATGGATTACTTATT 1975
796 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCATTTAATCGGTAGCGGCTTAATCAC 855
1976 GACTAAGTTAGGTAGGGAACAATCAACTCAGCTCATTTAATCGGTAGCGGCTTAATCAC 2035
856 CGGTAACCTTATCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACC 915
2036 CGGTAACCTTATCTATACGACTCACAGACTCAACTCTTGGGTATACAGGTAACTCTACC 2095
916 TTCAGTGGGAACCTAAATAATATCGGTGCGACCTACTTGGAAACCTTATCCGTAAGCAC 975
2096 TTCAGTGGGAACCTAAATAATATCGGTGCGACCTACTTGGAAACCTTATCCGTAAGCAC 2155
976 AACAGGGGATTTGCTCGGCACTTGTGCCAAAGTGGTGACACAGGTTCGGTTCTGTGAT 1035
2156 AACAGGGGATTTGCTCGGCACTTGTGCCAAAGTGGTGACACAGGTTCGGTTCTGTGAT 2215
1036 AGAAGAACTTTGACACCTCATCTGTATAGAACTGACTTAGATTATATTGTATCAAGAAT 1095
2216 AGAAGAACTTTGACACCTCATCTGTATAGAACTGACTTAGATTATATTGTATCAAGAAT 2275
1096 AGTAACGTTCCCTATGTCCTCGTATTTATTCCTGCTGAGCGGCAATACGTCCGCTG 1155
2276 AGTAACGTTCCCTATGTCCTCGTATTTTACTCTGCTTGGCGGCAATACATCGGCTG 2335
1156 TATGTACTCAAGACCGAAGCGGCACTTACTACACCATCATGACTATCAAGGTTCACT 1215
2336 TATGTACTCAAGACCGAAGCGGCACTTACTACACCATATATGACTATCAAGGCTCAGT 2395

1216 CATCGCAACTGCAAGATGACAACTATAGATGTAAACCCCGGGTATCATATCGCA 1275
2396 CATCGCTAACTGCAAGATGACAACTATAGATGTAAACCCCGGGTATCATATCGCA 2455
1276 AAATATGAGGAAGCCGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 1335
2456 AAATATGAGGAAGCCGTGTCTTAATAGATAAACAATCATGCAATGTTTTATCCTTAGG 2515
1336 CGGGATAAATTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT 1395
2516 CGGGATAAATTTAAGGCTCAGTGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT 2575
1396 ACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
2576 ACAAGATTTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 2635
1456 CAACAACCTGATCAGTAATGCTTTGTAATAGATTAGAGGAAGCAACAGAAACCTAGACAA 1515
2636 CAACAACCTGATCAGTAATGCTTTGTAATAGATTAGAGGAAGCAACAGAAACCTAGACAA 2695
1516 AGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATATCGTTTTGACTATCAT 1575
2696 AGTCAATGTCAAACTGACTAGCACATCTGCTCTCATTTACCTATATCGTTTTGACTATCAT 2755
1576 ATCTCTGTTTTGTTGTTACTTAGCCCTGATTTCTAGCATGCTTACCTAATGTACAAGCAAAA 1635
2756 ATCTCTGTTTTGTTGTTACTTAGCCCTGATTTCTAGCATGCTTACCTAATGTACAAGCAAAA 2815
1636 GGGCAACAAAAACCTTATTATGGCTTGGGAATATATCTCTAGATCAGATGAGGCCAC 1695
2816 GGGCAACAAAAACCTTATTATGGCTTGGGAATATATACCTAGATCAGATGAGGCCAC 2875
1696 TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTTAATAGTAATTTGTGTGAAG 1755
2876 TACAAAAATGTGAACACAGATGAGGAACGAAGGTTTCCCTTAATAGTAATTTGTGTGAAG 2935
1756 TTCTGTTAGTCTCTCAGTTTCAGAGAGTTTAAAGAAAAA 1792
2936 TTCTGTTAGTCTCTCAGTTTCAGAGAGTTTAAAGAAAAA 2972

RESULT 10

US-11-126-465-1
; Sequence 1, Application US/11126465
; Publication No. US20050202045A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Novel Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105K1OK
; CURRENT APPLICATION NUMBER: US/11/126,465
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/09/881,457
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1
; LENGTH: 3570
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1194)..(2888)
; OTHER INFORMATION: NDV Fusion Protein
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1355)
; OTHER INFORMATION: n = any nucleotide
US-11-126-465-1

Query Match      50.7%; Score 1701.6; DB 24; Length 3570;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

Qy 16 TGGATCCCGGTTGGCGCCCTCCAGGTGCAAGATGGGCTCCAGACCTTCTACCAAGAACCC 75
Db 1199 TCGATCCCGGTTGGCGCCCTCCAGGTGCGAGATGGGCTCCAGACCTTCTACCAAGAACCC 1258

Qy 76 AGCACTATGATGCTGACTATCCGGGTTGCGTGGCACTGAGTTGCATCTGTCCGGCAAA 135
Db 1259 AGCACTATGATGCTGACTATCCGGGTCGCGCTGCTGACTGAGTTGCATCTGTCCGGCAAA 1318

Qy 136 CTCATTGATGGCAGGCGCTCTTTCAGCTGCGAGGAATTGTGTTACAGGAGACAAAGCCGT 195
Db 1319 CTCATTGATGGCAGGCGCTCTTTCAGCTGCGAGG-ACTNTGGTTACAGGAGACAAAGCAAT 1377

Qy 196 CAACATATACAGCTCATCCGACGACGAGATCAATCATAGTTAAGTCTCTCCCGAATCTGCC 255
Db 1378 CAACATATACAGCTCATCCGACGACGAG--TCAATCATA--TTAAGTCTCTCCCGAATCTGCC 1435

Qy 256 CAAGGATAAGAGGAGGATGCGGAAGCCCTTGGATGCATACACAGGACATGAGCCAC 315
Db 1436 ANAGATAAGAGGAGGATGCGGAAGCCCTTGGATGCATACACAGGACATGAGCCAC 1495

Qy 316 TTTGCTACCCCGCTTGTGACTCTATCCGTAGGATACAAGAGTCTGTGACTACATCTGG 375
Db 1496 TTTGCTACCCCGCTTGTGACTCTATCCGTAGGATACAAGAGTCTGTGACTACATCTGG 1555

Qy 376 AGGGGGGAGACAGGGCGCCCTTATAGGCGCATTTATGGCGGTGTGGCTCTTGGGGTTC 435
Db 1556 AGGGGGGAGACAGGGCGCCCTTATAGGCGCATTTATGGCGGTGTGGCTCTTGGGGTTC 1615

Qy 436 AACTGCCGCAAAATAACAGCGCGCGAGCTCTGATACAAGCCAAACAAATGTCGCAA 495
Db 1616 AACTGCCGCAAAATAACAGCGCGCGAGCTCTGATACAAGCCAAACAAATGTCGCAA 1675

Qy 496 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGGTCACTGA 555
Db 1676 CATCTCCGACTTAAAGAGAGCATTTGCCGCAACCAATGAGGCTGTGCATGAGGTCACTGA 1735

Qy 556 CGGATATTCGCACTAGCAGTGGCAGTTTGGGAAGATGACAGGTTTGTAAATGACCAAT 615
Db 1736 CGGATATTCGCACTAGCAGTGGCAGTTTGGGAAGATGACAGGTTTGTAAATGACCAAT 1795

Qy 616 TAATAAACAGCTCAGGAATTAGCTGCATCAAAATTTGCAGCAAGTTGGTGTAGAGCT 675
Db 1796 TAATAAACAGCTCAGGAATTAGCTGCATCAAAATTTGCAGCAAGTTGGTGTAGAGCT 1855

Qy 676 CAACCTGTACCTAACCGAATTTAGCTACAGTATTCGACCAAAATCACTTCACCTGCTTT 735
Db 1856 CAACCTGTACCTAACCGAATTCAGTACAGTATTCGACCAAAATCACTTCACCTGCTTT 1915

Qy 736 AAAAAGCTGACTATTCAGGCACTTTACAATCTAGCTGGTGGAAATATGGAATTAAT 795
Db 1916 AAAAAGCTGACTATTCAGGCACTTTACAATCTAGCTGGTGGGAATATGGAATTAAT 1975

Qy 796 GACTAAGTGTAGGTAGGGAACAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 855
Db 1976 GACTAAGTGTAGGTAGGGAACAATCAACTCAGCTCATTAATCGGTAGCGGCTTAATCAC 2035
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RESULT 11

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US-10-838-834-19
; Sequence 19, Application US/10838834
; Publication No. US20050048074A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, et al.
; TITLE OF INVENTION: Vectors and Cells for Preparing Immunoprotective Compositions
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Qy 856 CGGTAAACCCCTATTTCTATACGACTCACAGACTCAACTCTTTGGGTATACAGGTAACCTCTACC 915
Db 2036 CGGTAAACCCCTATTTCTATACGACTCACAGACTCAACTCTTTGGGTATACAGGTAACCTCTACC 2095

Qy 916 TTCAGTCGGGAACCTTAAATAATATATCGTGCACACCTTCTTGGAAACCTTTATCCGTAAGCAC 975
Db 2096 TTCAGTCGGGAACCTTAAATAATATATCGTGCACACCTTCTTGGAAACCTTTATCCGTAAGCAC 2155

Qy 976 AACCAGGGGATTTGCTCGGCACCTTGTCCAAAAGTGTGACACAGGTCGGTCTTGTGAT 1035
Db 2156 AACCAGGGGATTTGCTCGGCACCTTGTCCAAAAGTGTGACACAGGTCGGTCTTGTGAT 2215

Qy 1036 AGAAGAACTTGACACCTCATATCTGTAATAGAAATCTGACTTTAGATTATATTGTACAAAGAT 1095
Db 2216 AGAAGAACTTGACACCTCATATCTGTAATAGAAATCTGACTTTAGATTATATTGTACAAAGAT 2275

Qy 1096 AGTAACGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGGCGGCAATACGTCCGCGCTG 1155
Db 2276 AGTAACGTTCCCTATGTCCTCGGTATTTATTCCTGCTTGGCGGCAATACGTCCGCGCTG 2335

Qy 1156 TATGTACTCAAGACCCGAGGCGCACTTACTACACCATATGACTATCAAAAGTTTCAGT 1215
Db 2336 TATGTACTCAAGACCCGAGGCGCACTTACTACACCATATGACTATCAAAAGTTTCAGT 2395

Qy 1216 CATCCCAACTGCAAGATGACAAATGATGTGTAAACCCCGGTATCATATCGCA 1275
Db 2396 CATCCCAACTGCAAGATGACAAATGATGTGTGTAAACCCCGGTATCATATCGCA 2455

Qy 1276 AAATATGAGAGACCGGCTGCTCTTAATAGATAAACAATCATGCAATGTTTATCCCTAGG 1335
Db 2456 AAATATGAGAGACCGGCTGCTCTTAATAGATAAACAATCATGCAATGTTTATCCCTAGG 2515

Qy 1336 CGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT 1395
Db 2516 CGGATTAACCTTAAAGGCTCAGTGGGGAATTCGATGTAACTTATCAGAAGAAATATCTCAAT 2575

Qy 1396 ACAAGATTTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 1455
Db 2576 ACAAGATTTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTTGGGAATGT 2635

Qy 1456 CAAACACTCGATCAGTAATGCTTTGTAAGTTAGAGAAAGCAACAGAACTAGACAA 1515
Db 2636 CAAACACTCGATCAGTAATGCTTTGTAAGTTAGAGAAAGCAACAGAACTAGACAA 2695

Qy 1516 AGTCAATGCTCAAACTGACTAGCACATCTGCTCTCAATACCTATATCGTTTGTGACTATCAT 1575
Db 2696 AGTCAATGCTCAAACTGACTAGCACATCTGCTCTCAATACCTATATCGTTTGTGACTATCAT 2755

Qy 1576 ATCTCTGTTTTTGGTATATCTAGCTGATTTAGCATGCTACCTTAATGTACAAGCAAAA 1635
Db 2756 ATCTCTGTTTTTGGTATATCTAGCTGATTTAGCATGCTACCTTAATGTACAAGCAAAA 2815

Qy 1636 GGCGCAACAAAACCTTATTTATGGCTTGGGAATAATATCTAGATCAGATGAGAGCCAC 1695
Db 2816 GGCGCAACAAAACCTTATTTATGGCTTGGGAATAATATCCCTAGATCAGATGAGAGCCAC 2875

Qy 1696 TACAAAATGTGAACACAGATGAGGACGAGGTTTCCCTAATAGTAATTTGTGTGGAAG 1755
Db 2876 TACAAAATGTGAACACAGATGAGGACGAGGTTTCCCTAATAGTAATTTGTGTGGAAG 2935

Qy 1756 TTCTGGTAGTCTGTCAAGTTCAAGAGAGTTTAAAGAAAAA 1792
Db 2936 TTCTGGTAGTCTGTCAAGTTCAAGAGAGTTTAAAGAAAAA 2972
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; TITLE OF INVENTION: Derived from Transgenic Plants

; FILE REFERENCE: 3121/2022

; CURRENT APPLICATION NUMBER: US/10/838,834

; CURRENT FILING DATE: 2004-05-04

; PRIOR APPLICATION NUMBER: US 60/467,998

; PRIOR FILING DATE: 2003-05-05

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 19

; LENGTH: 1734

; TYPE: DNA

; ORGANISM: Newcastle disease virus

; US-10-838-834-19

Query Match 42.7%; Score 1434.4; DB 21; Length 1734;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1438; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1915	ATGACCGCGCGCTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAAATACA	1974
Db	1	ATGACCGCGCGCTTAGCCAAAGTTGCGTTAGAGAAATGATGAAGAGAGGCAAAAATACA	60
Qy	1975	TGGCGCTTGATATCCGGATTGCAATCTTATCTTAAACAGTAGTGAACCTTGGCTATATCT	2034
Db	61	TGGCGCTTGATATCCGGATTGCAATCTTATCTTAAACAGTAGTGAACCTTGGCTATATCT	120
Qy	2035	GTAGCCCTCCCTTTATATAGCATGGGGCTAGCACACTAGCGATCTTGTAGGCATACCG	2094
Db	121	GTAGCCCTCCCTTTATATAGCATGGGGCTAGCACACTAGCGATCTTGTAGGCATACCG	180
Qy	2095	ACTAGGATTTCCAGGCGAGAAAGATTACATCTACACTTGGTTCGAATCAAGATGTA	2154
Db	181	ACTAGGATTTCCAGGCGAGAAAGATTACATCTACACTTGGTTCGAATCAAGATGTA	240
Qy	2155	GTAGATAGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCAATGTTAAATCTGAG	2214
Db	241	GTAGATAGGATATATAAGCAAGTGGCCCTTGAGTCTCCGTTGGCAATGTTAAATCTGAG	300
Qy	2215	ACCACATTTAGACGCAATTAACATCTCTCTTATCAGATTATGAGCTGCGCAACAC	2274
Db	301	ACCACATTTAGACGCAATTAACATCTCTCTTATCAGATTATGAGCTGCGCAACAC	360
Qy	2275	AGTGGGTGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGACTC	2334
Db	361	AGCGGTGGGGGCGACCTATCCATGACCCAGATTATATAGGGGGGATAGGCAAAAGACTC	420
Qy	2335	ATTGTAGATGATGTAGTAGTGCATCATCTTATCCCTCTGCAATTTCAAGAACATCTG	2394
Db	421	ATTGTAGATGATGTAGTAGTGCATCATCTTATCCCTCTGCAATTTCAAGAACATCTG	480
Qy	2395	AAATTTATCCCGCGCCTTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATG	2454
Db	481	AAATTTATCCCGCGCCTTACTACAGGATCAGGTTGCACTCGAATACCCCTCATTTGACATG	540
Qy	2455	AGTGCTACCCATTTACTGTACACCCATTAATGTAATTTGTCTGGATGAGAGATCACTCA	2514
Db	541	AGTGCTACCCATTTACTGTACACCCATTAATGTAATTTGTCTGGATGAGAGATCACTCA	600
Qy	2515	CATTATATCATGATTTAGCATCTTGGTGTCTCCGGACATCTGCAACAGGAGGGATTC	2574
Db	601	CATTATATCATGATTTAGCATCTTGGTGTCTCCGGACATCTGCAACAGGAGGGGGTATTC	660
Qy	2575	TTTTCTACTCTGCGTTCCATCAACTGTGACACACCCCAAAATCGGAAGTCTTGCAGTGTG	2634
Db	661	TTTTCTACTCTGCGTTCCATCAACTGTGACACACCCCAAAATCGGAAGTCTTGCAGTGTG	720
Qy	2635	AGTGCAACTCCCTTGGGTGTGATATGCTGTGCTCGAAAGTCACGGAGACAGAGAA	2694
Db	721	AGTGCAACTCCCTTGGGTGTGATATGCTGTGCTCGAAAGTCACGGAGACAGAGAA	780
Qy	2695	GATTATAACTCAGCTGTCCCTACCGGGATGTAATCATGGAGGTTAGGGTTCGACGGCCAG	2754
Db	781	GATTATAACTCAGCTGTCCCTACCGGGATGTAATCATGGAGGTTAGGGTTCGACGGCCAG	840

Qy	2755	TACCACGAAAAGGACCTAGATGTCAACAATTATTTCGGGGAAGTGGGTGGCAACTACCCA	2814
Db	841	TACCACGAAAAGGACCTAGATGTCAACAATTATTTCGGGGAAGTGGGTGGCAACTACCCA	900
Qy	2815	GGAGTAGGGGTGGATCTTTTATTGACAGCGCGTATGGTTCTCAGTCTACGGAGGGTTA	2874
Db	901	GGAGTAGGGGTGGATCTTTTATTGACAGCGCGTATGGTTCTCAGTCTACGGAGGGTTA	960
Qy	2875	AAACCCAAATTCACCCAGTGCACCTGTACAGAGGGAATATGTATATCAACGGATAC	2934
Db	961	AAACCCAAATTCACCCAGTGCACCTGTACAGAGGGAATATGTATATCAACGAATAC	1020
Qy	2935	AATGACACATGCCAGATGAGCAAGACTACACAGATTCGAATGGCAAGTCTTCTGATAAG	2994
Db	1021	AATGACACATGCCAGATGAGCAAGACTACACAGATTCGAATGGCAAGTCTTCTGATAAG	1080
Qy	2995	CCTGAGCGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACA	3054
Db	1081	CCTGAGCGGTTTGGTGGGAAACGCATACAGCAGGCTATCTTATCTATCAAGGTGTCAACA	1140
Qy	3055	TCCTTAGGCGAAGACCGGTACTGACTGTACCGCCCAACACAGTCACACTCATGGGGCC	3114
Db	1141	TCCTTAGGCGAAGACCGGTACTGACTGTACCGCCCAACACAGTCACACTCATGGGGCC	1200
Qy	3115	GAAGCGAAGATTTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATAC	3174
Db	1201	GAAGCGAAGATTTCTCAGTAGGACATCTCATTTCTTGTATCAACGAGGTCATCATAC	1260
Qy	3175	TTCTCTCCCGGTTTATATATCCATGACAGTACAGCAACAAACAGGCACCTCTTCTAGT	3234
Db	1261	TTCTCTCCCGGTTTATATATCCATGACAGTACAGCAACAAACAGGCACCTCTTCTAGT	1320
Qy	3235	CTTTATACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGGCAGGCTTCAGCAAGA	3294
Db	1321	CTTTATACATTCATGCTTCACTCGGCCAGGTAGTATCCCTTGGCAGGCTTCAGCAAGA	1380
Qy	3295	TGCCCCAACTCGTGTGTTACTTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGA	3354
Db	1381	TGCCCCAACTCGTGTGTTACTTGGAGTCTATACAGATCCATATCCCTTAATCTTCTATAGA	1440
Qy	3355	AACC 3358	
Db	1441	AACC 1444	

RESULT 12

US-10-725-841-1

; Sequence 1, Application US/10725841

; Publication No. US20040131640A1

; GENERAL INFORMATION:

; APPLICANT: Geerlings, Harmen J.

; APPLICANT: Brown, Ian H.

; APPLICANT: Alexander, Dennis J.

; APPLICANT: Collins, Michael S.

; TITLE OF INVENTION: Escape Mutants of Newcastle Disease Virus as Marker Vaccines

; FILE REFERENCE: AM100044

; CURRENT APPLICATION NUMBER: US/10/725,841

; CURRENT FILING DATE: 2003-12-02

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 1662

; TYPE: DNA

; ORGANISM: Paramyxovirus/Newcastle Disease Virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1662)

US-10-725-841-1

Query Match 42.1%; Score 1414; DB 19; Length 1662;

Best Local Similarity 90.7%; Pred. No. 0;

Matches 1507; Conservative 0; Mismatches 155; Indels 0; Gaps 0;


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QY 47 ATGGGCTCCAGACCTTCTACCAAGAACCCAGACACCTATGATGCTGACTATATCCGGGTTGG 106
Db 1 ATGGGCTCCAGATCTTCTACCAAGGATCCAGGATACCTCTGATGCTGACCGTCCGGGTCGG 60
QY 107 CTGGCACTGAGTTGCATCTGTCCGCAAACTCCATTTGATGGCAGGCTCTTTGACGCTCA 166
Db 61 CTGGCACTGAGTTGCGTCTGTCCGCAAACTCCATTTGATGGCAGGCTCTTTGACGCTCA 120
QY 167 GGAATTGTGGTTPACAGGAGACAAAGCCGTCAACATATACACCTCATCCAGACAGGATCA 226
Db 121 GGAATTGTGGTGACAGGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTC 180
QY 227 ATCATAGTTAAGCTCTCTCCGAACTCTGCCAAGGATAGGAGGATGTGCGAAAGCCGCC 286
Db 181 ATCATAGTCAAGTTACTCTCCCAATATGCCCAAGATAAAGAGGCGTGTGCAAAAGCCGCC 240
QY 287 TTGGATGCATACAAACAGACATTTGACCTTTGCTCACCCCTTTGGTGACTCTATCCGT 346
Db 241 TTGGAGGCGTACACAGGACATTTGACTTTTGCTCACCCCTTTGGTGATTTCTATTCT 300
QY 347 AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGCGGCTTTATAGCGCC 406
Db 301 AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGAAACAGGGACGCTTTATAGCGCC 360
QY 407 ATTATGGCGGTGTGGCTCTTGGGTTTGGAACTGCGCGCAAAATTAACAGCGGCGCAGCT 466
Db 361 ATTATCGCGGTGCAGCTCTCGGGTTGCAACCGCTGCACAGATTAACAGCAGCTTCGGCT 420
QY 467 CTGATACAAGCCAAACAAATGCTGCCAACATCTCCGACTTAAAGAGAGCATTTGCCGA 526
Db 421 CTGATACAAGCCAAACAAATGCTGCCAACATCTCCGCTTAAAGAGAGAAATTTGCTCA 480
QY 527 ACCAATGAGGCTGTGCATGAGTCACTGACGGAATTCGCAACTAGCAGTGCGAGTTGG 586
Db 481 ACCAATGAGGCTGTGCACAGGCTCACTGATGATTAACAACACTAGCAGTTGG 540
QY 587 AAGATGACAGCTTTGTTTAAGCAAAATTAATAAAACAGCTCAGGAATTAAGATGCAATC 646
Db 541 AAGATGACAGCAATTTGTTTAAGCAGATTAATAAAACAGCTCAGGAATTTGACTGTATA 600
QY 647 AAAATTCACACGAGTTGGTGTAGAGCTCAACCTGTACCTTAACCGAATTCAGCTACAGTA 706
Db 601 AAAATTCACACGAGTTGGTGTAGAGCTCAACCTGTATCTAACTGAATTAAGCTACAGTA 660
QY 707 TTCGACACCAAAATCACTTCACTCTCTTTAAACAGAGTCACTATTTCAGGCACTTTACAAT 766
Db 661 TTCGACACCAAAATCACTTCCCTCTCTTTAACCCAGCTGACTATCCAGGCGCTTTACAAT 720
QY 767 CTAGCTGTGGAAATATGGAATTAATGACTAAGTTAGGTAGGTAGGAAACAATCAACTC 826
Db 721 CTAGCTGTGGGAATATGGAATTAATGACTAAGTTAGGTAGGTAGGAAACAATCAACTC 780
QY 827 AGCTCATTAATCGGTAGCGGCTTAATCACCGTAACCTTATCTATACGACTCACAGACT 886
Db 781 AGCTCATTAATCGGTAGCGGCTGATCACCGCAACCTTATCTGTACGACTCACAGACT 840
QY 887 CAACCTCTGGGTATACAGTAACTCTACCTTCAGTCGGGAACCTAAATAATATGCGTCC 946
Db 841 CAGCTCTTTGGGTATACAGTAACTCTACCTTCAGTCGGGAACCTGAATTAATATGCGTCC 900
QY 947 ACCTACTTTGGAACCTTTATCCGTAGCAACAACCCAGGGGATTTGCTCCGCACTTTGTCCA 1006
Db 901 ACCTACTTTGGAACCTTTGCTGTAGTAACTAAACCAAGGATTTGCTCAGCACTGTGTCCA 960
QY 1007 AAAGTGTGACACAGGTCGGTCTGTGATAGAGAACTTGACACTCATCTGATATAGAA 1066
Db 961 AAAGTGTGATGAAGGTCGGTTCGGTATAGAGAACTTGACACTCATCTGATATAGAA 1020
QY 1067 ACTGACTTTAGATTTATATTTGATCAAGAATAGTAAGCTTCCCTATGTCCTCCCTGGTATTTAT 1126
Db 1021 ACCGATTTGGATCTATATTTGATCAAGAATAGTGACATTTCCCTATGCTCTCTGGTATTTAT 1080
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QY 1127 TCCTGCTTGAGGGCAATACGTCCGCCCTGTATGTACTCAAGACCGAAGGCGCACTTACT 1186
Db 1081 TCCTGCTTGAGGGCAATACATCCGCTTTGCATGTACTCGAAGCTGAAGGCGCACTCACT 1140
QY 1187 ACACCATATCATGACTATCAAAAGTTTCAGTCAATCGCAACTGCAAGATGACAACATGTAGA 1246
Db 1141 AGCGGTATCATGACTCTCAAAAGCTCAGTTATTGCAACTGTAAAGTACAAACATGTAGA 1200
QY 1247 TGTGTAAACCCCGGGTATCATATCGCAAACTATGAGAGAGCGGTGTCTTAATAGAT 1306
Db 1201 TGTGCAGACCCCGGGTATCATATCGCAAAATTAATGAGAGAGCTGTGTCTCTAATAGAT 1260
QY 1307 AAACAATCATCAATGTTTTTATCCTTAGCGGGATACTTTTAAGGCTCAGTGGGAAATTC 1366
Db 1261 AGGCAATCATGCAATGTCTTATCCTTAGACCGGAATACTTTGAGGCTCAGTGGGAAATTT 1320
QY 1367 GATGTAACTTATCAAGAATAATCTCAATACAAGATTTCTCAAGTAAATAATAACAGGCAAT 1426
Db 1321 GATGCACTTATCAAGAATAATCTCAATACAAGATTTCTCAAGTAAATAATAACAGGCAAT 1380
QY 1427 CTTGATATCTCAACTGAGCTTTGGGAATGTCAAACTCGATCAGTAAATGCTTTGAATAG 1486
Db 1381 CTCGATATCTCGACTGAGCTTTGGGAATGTCAAACTCGATCAGTAAATGCTTTGAATAG 1440
QY 1487 TTAGAGGAAGCAACAGAAAAGTACAGAACTCAATGTCAAACTGACCTAGACATCTGCT 1546
Db 1441 TTAGAGGAAGCAACAGAAAAGTACAGAACTCAATGTCAAACTGACCTAGACATCTGCT 1500
QY 1547 CTCATTACTATATCGTTTTTTCAGTATCATATCTCTTTGTTTTTGGTATATCTTAGCCTGATT 1606
Db 1501 CTCATTACTATATCGTTTTTTCAGTATCATATCTCTTTGTTTTTGGTATATCTTAGCCTGATT 1560
QY 1607 CTAGCATCTACCTAAATGTACAAGCAAAAGGCGCAACAAAAACCTTATTATGGCTTGG 1666
Db 1561 CTAGCATCTACCTAAATGTACAAGCAAAAGGCGCAACAAAAACCTTATTATGGCTTGG 1620
QY 1667 AATAATCTCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1708
Db 1621 AATAATCTCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1662
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RESULT 13

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US-10-990-204-1
; Sequence 1, Application US/10990204
; Publication No. US20050069561A1
; GENERAL INFORMATION:
; APPLICANT: Geerligs, Harmen J.
; APPLICANT: Brown, Ian H.
; APPLICANT: Alexander, Dennis J.
; APPLICANT: Collins, Michael S.
; TITLE OF INVENTION: Escape Mutants of Newcastle Disease Virus as Marker Vaccines
; FILE REFERENCE: AM10004
; CURRENT APPLICATION NUMBER: US/10/990,204
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Paramyxovirus/Newcastle Disease Virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1662)
US-10-990-204-1
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Query Match 42.1%; Score 1414; DB 21; Length 1662;

Best Local Similarity 90.7%; Pred. No. 0;

Matches 1507; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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QY 47 ATGGGCTCCAGACCTTCTTACCAAGAACCCAGACACCTATGATGCTGACTATATCCGGGTTGG 106
Db 1 ATGGGCTCCAGATCTTCTACCAAGGATCCAGGATACCTCTGATGCTGACCGTCCGGGTCGG 60
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Qy 107 CTGCACTGAGTGTGCTATCTGTCGCGCAAACTCCATATGATGGCAGCGCTTCTTGACAGTGA 166
Db 61 CTGCACTGAGTGTGCTATCTGTCGCGCAAACTCCATATGATGGCAGCGCTTCTTGACAGTGA 120
Qy 167 GGAATTGTGGTTA CAGGAGACAAGCGGTCAACATATACCTCATCCGACAGGATCA 226
Db 121 GGGATTGTGGTTGACAGGAGACAAGCGGTCAACATATACCTCATCCGACAGGATCA 180
Qy 227 ATCATAGTTAGCTCTCCGGAATCTGCCAAGATGAAGGAGGATGTGGGAAAGCCCC 286
Db 181 ATCATAGTTAGCTCTCCGGAATGTGCCAAGATGAAGGAGGATGTGGGAAAGCCCC 240
Qy 287 TTGGATGCATACACAGGACATTTGACCACTTTGCTCACCCCCCTTGTGTGACTCTATCCGT 346
Db 241 TTGGAGGCGTACAACAGGACATTTGACTTCTTGTCTCACCCCCCTTGTGTGACTCTATCCGT 300
Qy 347 AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGGAGACAGGGCGCGCTTATAGGGGCC 406
Db 301 AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGGAAACAGGGCGCGCTTATAGGGGCC 360
Qy 407 ATTATTTGGCGGTGGCTCTTGGGGTTGCCAATCTCCGCACTCCGCAAAATAACAGCGCGCGAGCT 466
Db 361 ATTATCGCGGTGAGCTCTCGGGGTTGCCAATCTCCGCACTCCGCAAAATAACAGCGCGCTTCGGCT 420
Qy 467 CTGATACAAGCAAAATGCTGCCAATCTCCGCACTTAAAGAGAGCAATTCGCGCA 526
Db 421 CTGATACAAGCAAAATGCTGCCAATCTCCGCACTTAAAGAGAGCAATTTGCTGCA 480
Qy 527 ACCAATGAGGTGTGCTAGAGTCACTGACCGATTTATCGCAATTCGCAATTCGCAATTCGCA 586
Db 481 ACCAATGAGGTGTGCTAGAGTCACTGATGGATTTATCACTAGCAGTGGCAGTTGGG 540
Qy 587 AAGTGCAGCAGTTTGTAAATGACCAATTTAATAAAGAGCTCAGGAATTTAGCTGCATC 646
Db 541 AAGTGCAGCAGTTTGTAAATGACCAATTTAATAAAGAGCTCAGGAATTTGACTGTATA 600
Qy 647 AAAATTGCACAGCAAGTTGGTTAGAGCTCAACCTGTACCTAACCGAATTTGACTTACAGTA 706
Db 601 AAAATTACCAGCAGTTGGTTAGAGCTCAACCTGTATCTAATCTAATTTGACTTACAGTA 660
Qy 707 TTGCGGACCAAAATCACTTCCCTGCTTAAACAGCTGACTATTTAGGCACTTTACAT 766
Db 661 TTGCGGACCAAAATCACTTCCCTGCTTAAACAGCTGACTATTTAGGCACTTTACAT 720
Qy 767 CTACTGTTGGAATATGGAATTTACTTATTTAGTAACTTGTAGTGTAGGGAACAATCACTC 826
Db 721 CTACTGTTGGAATATGGAATTTACTTATTTAGTAACTTGTAGTGTAGGGAACAATCACTC 780
Qy 827 AGCTCATTAATCGGTAGCGGCTTAAATCACCGGTAAACCTTATTTATACGACTCACAGCT 886
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Db 1141 ACGCCGTACATGACTCTCAAAAGGCTCAGTTATTATTCGCAACTGTAAAGATGACAACTGTAGA 1200
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Db 1201 TGTGCAAGCCCGGGGTATCATATCGCAAACTATGGAAGAGCTGTCTCTTAATAGAT 1260
Qy 1307 AAACAATCATGCAATGTTTTATCCTTAGGGGGGATAACTTTAAGGCTCAGTGGGGAAATTC 1366
Db 1261 AGCAATCATGCAATGTCCTATCCTTAGACGGAATACTTTGAGGCTCAGTGGGGAAATTT 1320
Qy 1367 GATGTAACCTTATCAGAAAGATATCTCAATACAGATTTCTCAAGTAATAATAACAGGCAAT 1426
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Qy 1487 TTAGAGAAAGCAACAGAAACTAGACAAAAGTCAATGTCAAACTGACTAGCACATCTGCT 1546
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Qy 1667 AATAATATCTTAGATCAGATCAGAGCCACTACAAAAATGTGA 1708
Db 1621 AATAATATCTTAGATCAGATCAGAGCCACTACAAAAATGTGA 1662

RESULT 14
US-09-784-990-10
; Sequence 10, Application us/09784990
; Patent No. US20020037292A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/784,990
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-09-784-990-10

Query Match 40.6%; Score 1362.8; DB 9; Length 1662;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

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Qy 167 GGAATTGTGGTTACAGGAGCAAAAGCCGCTCAACATATACCTCATCCAGACAGGATCA 226

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587 AAGATGACAGCAGTTTGTAAATGACCAATTTAATAAAGCAGCTCAGGAATTAAGACTGCATC 646
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721 CTAGCTGTGGAAATATGATTTACTTTTAACTAGTGTAGGTAGGGAACAAATCAATC 780
827 AGCTCAATTAATCGGTAGCGGTAAATACCGGTAAACCTTATCTATACGACTCACAGACT 886
781 AGCTCAATTAATCGGTAGCGGTAAATACCGGTAAACCTTATCTATACGACTCACAGACT 840
887 CAACCTTTGGGTATACAGGTAACCTTACTTCACTGCGGAACTTAATTAATATGCGTCC 946
841 CAGATCTTTGGGTATACAGGTAACCTTACTTCACTGCGGAACTTAATTAATATGCGTCC 900
947 ACCTACTTTGGAAACCTTATCGGTAAAGCAACACCGGGATTTGCCCTCGGCACTTGTCCCA 1006
901 ACCTACTTTGGAAACCTTATCTGTAAAGCAACACCGGGATTTGCCCTCGGCACTTGTCCCA 960
1007 AAAGTGTGACACAGGTCCGTCTGTGTATAGAGAACTTGACACTCATACTGTATAGAA 1066
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1067 ACTGACTTTAGATTTATTTATGATACAGAAATAGTAAGTTTCCCTATGTCCTCGGTATTTAT 1126
1021 ACCGACTTTGGATTTATTTATCTGTACAGAAATAGTGACATTTCCCTATGTCCTCGGTATTTAT 1080
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1081 TCTGTCTGAGCGGTAATACATCGGCTTGATGTATTTCAAGACTGGAAGGCGCACTTACT 1140
1187 ACACCATACATGACTATCAAGAGTTTCACTCATCGCAATCTGCAAGATGACAAATGTAGA 1246
1141 ACGCATATATGGCTCTCAAGAGCTCAGTTATTTGCAATTTGCAAGCTGCAACATGTAGA 1200
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1201 TGTGAGATCCCCAGGTATCATATCGCAAAATTTATGGAGAGCTGTGTCTTAAATAGAT 1260
1307 AAAACAATCATGCAATGTTTTTATCTTATAGGCGGATAAATTTTAAAGCTCAGTGGGAAATTC 1366
1261 AGGCACTCATGCAACGTCTTATCTTATAGCGGATAAATCTGAGGCTCAGTGGGAAATTT 1320
1367 GATGTAACCTTATCAGAAGAAATATCTCAATACAAGATTCTCAAGTAATATACAGGCAAT 1426
1321 GATGCAACCTTATCAAAAGAAATATCTCTATATAGTAATCTCAAGTTTATAGTGACAGGCAAT 1380
1427 CTTGATATCTCAACTGAGCTTTGGGAATGTCAACAACTCGATCAGTAATGCTTTTGAATAG 1486
1381 CTTGATATCAACTGAGCTTTGGGAATGTCAACAACTCAATAGTAATGCTTGAATAG 1440
1487 TTAGAGAAAGCAACAGAAACTAGACAAAGTCAATGTCAAACTCACTAGACATCTGCT 1546
1441 TTAGAGAAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCACTGCT 1500
1547 CTCATTACTATATCGTTTTCAGTATCATATCTCTGTTTGGTATATCTTAGCCCTGATT 1606
1501 CTCATTACTATATCGTTTTCAGTATCATATCTCTGTTTGGTATATCTTAGCCCTGATT 1560
1607 CTAGCATCTACCTAAATGTACAAGCAAAAGCGCAACAAACCTTATTTATGCTTGGG 1666
1561 CTAGCATCTACCTAAATGTACAAGCAAAAGCGCAACAAACCTTATTTATGCTTGGG 1620
1667 AATAATCTCTAGATCAGATGAGAGCCACTACAAAATGTGA 1708
1621 AATAATACCTTTGATCAGATGAGAGCCACTACAAAATATGA 1662

RESULT 15

US-10-229-412-10
; Sequence 10, Application US/10229412
; Publication No. US20030124145A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/10/229,412
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/232,479
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-10-229-412-10

Query Match 40.6%; Score 1362.8; DB 15; Length 1662;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1475; Conservative 0; Mismatches 187; Indels 0; Gaps 0;
47 ATGGGCTCCAGACCTTTTACCAAGAACCCAGACACTATGATGCTGACTATCCGGGTGGG 106
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167 GGAATTGTTGTTACAGGAGACAAAGCCCTCAACATATACACTATCCAGACAGATCA 226
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Db 241 TTGGAGGCATACAAACAGGACACTGACTACTTTTACTCACCCGCCCTTGTGTGATTTCTATCCGC 300
QY 347 AGGATACAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGCGCCCTTATAGGCGCC 406
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QY 827 AGCTCATTAATCGGTAGCGGCTTAATCACCGGTAAACCCCTATTCTATACGACTCAAGACT 886
Db 781 AGCTCATTAATTGGTAGCGGCTTGATCACCGGCAACCCCTATTCTGTACGACTCAAGACT 840
QY 887 CAATCTTTGGGTATACAGGTAACCTACTACTTTCAGTCGGGAACCTTAATAATATGGTGCC 946
Db 841 CAGATCTTTGGGTATACAGGTAACCTTTGCTTTTCAAGTGGGAACTTGAATAATATGGTGCC 900
QY 947 ACCTACTTTGGAAACCTTATCCGTAAAGCAACACAGGGGATTTGCTCGGCACTTTGTCCCA 1006
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QY 1007 AAAGTGGTGACACAGGTGCGTCTGTGTAGTAGAAGAACTTGCACCTCATACTGTATAGAA 1066
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Db 1621 AATAAATACCTTGTATCAGATGAGAGCCACTACAAAAATATGA 1662
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	46.2	1.4	886	AZ541254	AZ541254 ENTFALLTF
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6	43.2	1.3	386	AW329422	AW329422 NC00657e
7	43.2	1.3	494	AL380807	AL380807 MCB854F09
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10	42.4	1.3	507	CD081007	CD081007 MA3-999SU
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c 27	40.4	1.2	801	9	BX213898	BX213898	Danio rer
c 28	40.2	1.2	779	8	AQ855008	AQ855008	CpG2055B
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c 35	40	1.2	1086	9	CNS00YXK	AL096962	Drosophil
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c 38	39.8	1.2	584	9	CR484222	CR484222	Medicago
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c 41	39.8	1.2	764	9	CG932090	CG932090	MBECD44TR
c 42	39.8	1.2	868	9	CG924570	CG924570	MBEAB79TR
c 43	39.6	1.2	567	9	CR346391	CR346391	Medicago
c 44	39.6	1.2	580	8	AZ583873	AZ583873	1M0388J04
c 45	39.6	1.2	913	9	CNS04HG7	AL290896	Tetraodon

ALIGNMENTS

RESULT 1
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DEFINITION SSH227 SSH generated forward (3 days-2 days) subtracted cDNA
Library Phanerochaete chrysosporium cDNA, mRNA sequence.
ACCESSION CK280174
VERSION CK280174.1 GI:40556623
KEYWORDS EST.
SOURCE Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)
ORGANISM Phanerochaete chrysosporium
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Corticiaceae; Phanerochaete.
REFERENCE 1 (bases 1 to 766)
AUTHORS Jiang,M. and Zhang,Y.
TITLE Screen for Temporal-specific Expression Genes of Phanerochaete
chrysosporium Based on SSH and cDNA Microarrays
JOURNAL Unpublished (2003)
COMMENT Contact: Yizheng Zhang
Sichuan Key Laboratory of Molecular Biology and Biotechnology
College of Life Science, Sichuan University
Chengdu, Sichuan, box610064 P.R.CHINA
Tel: 86 028 85412738
Email: yizhang@scu.edu.cn

SSH generated forward (3 days-2 days) subtracted cDNA library of
Phanerochaete chrysosporium; average insert size:600 bp;
information: Isolation of total RNA from the mycelia incubated in
shallow stationary culture (Kirk media) at 39_
Insert Length: 766 Std Error: 0.00
POLYA-No.

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/db_xref="taxon:5306"
/clone_lib="SSH generated forward (3 days-2 days)
subtracted cDNA library"
/note="Vector: pMD18T-vector; SSH generated cDNA library
of Phanerochaete chrysosporium incubated in N-limited
shallow stationary culture"

ORIGIN

Query Match 14.9%; Score 500.8; DB 7; Length 766;
Best Local Similarity 84.1%; Pred. No. 7,4e-137;
Matches 565; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
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Qy 103 TGCCTGGCACTGAGTTGCTATCTGTCCGCAAACTCCATGATGCGAGGCTCTTTGAGC 162
Db 155 TATGCTGATATTGGCTGTATCCGTCGCAAAAGCTCTTTGACGCGAGGCTCTTTGAGC 214
Qy 163 TGCAGGAATTGTGTTACAGAGACAAAGCGCTCAATATATACACCTTCATCCGAGAG 222
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Qy 223 ATCAATCATAGTTAAAGTCTCTCCGAATCTGCCAAAGATAAGGAGGATGTGCGAAAGC 282
Db 275 GTCAATCATAGTCAAGTTGCTCCGATATATGCCAGGATAGAGGCGGTGTGCGAAAGC 334
Qy 283 CCCCTTGGATCATACACAGGACATTTGCTCAACCTTTGCTCAACCCCTTTGCTGACTTAT 342
Db 335 CCCATTAGAGCATATAACAGAACACTGACTACTTTGCTCACTCTCTTTGGCGACTCCAT 394
Qy 343 CCGTAGGATCAAGAGTCTGTGACTACATCTGGAGGGGGGAGACAGGGGGCCCTTATAGG 402
Db 395 CCGCAAGATCCAAAGGCTGTGTCCAGTCTGAGGAGGAGAGCAAAAACGCTTTATAGG 454
Qy 403 CGCCATTATTGGCGGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATAACAGGCGCGC 462
Db 455 TGCTGTTATTGGCGGTGTAGCTCTTGGGTTGCAACAGCGGCACAGATAACAGCAGTGC 514
Qy 463 AGCTCTGATACAGCCCAAAATAATGTGCAACATCTCCGACTTAAAGAGAGCATTCG 522
Db 515 GGCCCTAATACAGCCCAACCGAATGCCGCAACATCTCCGGCTTAAAGGAGAGCATTCG 574
Qy 523 CGCAACCAATGAGCTGTGATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGT 582
Db 575 TGCAACCAATGAAGCTGTGATGAAGTCAACGACGGATTTATCGCAACTATCAGTGGCAGT 634
Qy 583 TGGGAAGATGACGAGTTTGTATGACCAATTTAATAAAGACGTCAGGAATTTAGACTG 642
Db 635 TGGGAAGATGACGAGTTTGTCAATGACGAGTTTAAATATAGCGCGGAGAAATTTGAGCTG 694
Qy 643 CATCAAAATTGCACAGCAAGTTGTGTAGAGCTCAACCTGTACCTTAACCGAAATTTGACTAC 702
Db 695 TATAAAATCACACACAGGTTGGTTAGTAAGTCAACCTATACCTTAACCTGAATTTGACTAC 754
Qy 703 AGTATTGGGACC 714
Db 755 AGTATTGGGACC 766
```

RESULT 2
BG661033
LOCUS N339 SSH-HCA-U library Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BG661033
VERSION BG661033.1 GI:13805211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)
Zhang,Z. and DuBois,R.N.
Detection of differentially expressed genes in human colon cancer cells treatment with NS-398 using suppression subtractive hybridization and differential screening
Unpublished (2000)
Contact: Zhonghua Zhang
Department of Medicine
Vanderbilt Medical Center
MCN C-2104, 1161 21st Ave. South, Nashville, TN 37212, USA
Tel: 615 343 1369
Fax: 615 343 6229
Email: zhonghua.zhang@mcmail.vanderbilt.edu
DNA sequencing by: Vanderbilt Medical Center DNA sequencing core

laboratory. This is a fragment of gene that up-regulated by NS-398 treatment.
PCR Primers
FORWARD: 5'-CTAATAGCACTCACTATAGGC-3'
BACKWARD: 5'-TCGAGCGCCGCCGGCAGGT-3'
Seq primer: M13 forward primer
High quality sequence stop: 692.
FEATURES
Location/Qualifiers
1..692
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="Colon cancer cell"
/cell_line="HCA-7"
/clone_lib="SSH-HCA-U library"
/notes="Vector: PCR2.1-TOPO; Poly A RNA was isolated from NS-398 treated and control cells, and suppression subtractive hybridization was performed in forward and reverse directions. The adapter sequences used in the hybridization were as follows:
5'-CTAATAGCACTCACTATAGGCCTCGAGCGCGCCCGGCGAGGT-3'
(adapter 1) and
5'-CTAATACGACTCACTATAGGCGACGCTGTGTCGGGCGCAGGT-3' (adapter 2)."

ORIGIN
Query Match 2.6%; Score 87.8; DB 4; Length 692;
Best Local Similarity 48.7%; Pred. No. 6.3e-14;
Matches 273; Conservative 0; Mismatches 282; Indels 6; Gaps 1;
Qy 219 CAGGATCAATCATAGTTAAGCTCTCCGAATCTGCCAAGGATAAGGAGCATGTGCGA 278
Db 132 CAGATTCATTTGTTGAAGTTAATGCTACATTTGACTGCCGATTTAGTGATTAATA 191
Qy 279 AAGCCCCCTTGGATGCATACACAGGACATTTGCTCACCCCCCTTGGTGAAT 338
Db 192 TAACATCAATTTCAAGCTATAATGCAACAGTGACAAATCTTACAGCGATCGTGAGA 251
Qy 339 CTATCCGTAGATACAGAGTGTGTGACTACATCTGGAGGGGGAGACAGGGGCGCTTA 398
Db 252 ATTTGGAGACAAATTTAGAACCCAGTTTGAATCCAACT-----CGGAGGAGACGCCGATTTG 305
Qy 399 TAGCGCCATTATTGGCGGTGTGGCTCTTGGGGTTGCAACTGCCGCAAAATAACAGCGG 458
Db 306 CAGGGGTGTGATTTGGATTAGCTGATTTAGGATGAGTACTGCGCGACAGCTCACTGCCG 365
Qy 459 CCGCAGCTCTGATACAAAGCCAAACAAATGCTGCCACATCTCTCCGACTTAAAGAGAGCA 518
Db 366 CAGTAGCACTAGTAAAGGCAAAATGAAAATGCTGGCGGTACTCAATCTCAAAAATGCAA 425
Qy 519 TTGCCGCAACCATGAGGCTGTGATGAGTCACTGAGGATTTATCGCAACTAGCAGTGG 578
Db 426 TCCAAAAAACAATGCGGCAAGTTTCAGACGTTGTCAGAGGCCACACAATCACTAGGAACGG 485
Qy 579 CAGTTGGGAAGATGACGAGTTTCTTAATGACCAATTTAATAAACAAGCTCAGGAATTAG 638
Db 486 CAGTTCAAGCAGTTCAAGATCATATAACAGTGTGTAAGTCCAGCAATTACACAGCCA 545
Qy 639 ACTGCATCAAAATTTGCACAGCAAGTTGGTGTAGAGCTCAACCTGTACTACCAACCAATTGA 698
Db 546 ACTTAAGGCCCAAGATGCTATCATTTGGCTCAATCTCAATCTCTATTGACCGAGTTGA 605
Qy 699 CTACAGTATTTCGACCAAAATCACTTCACTGCTTTTAAACAAGCTGACTATTTAGGCAC 758
Db 606 CAATATCTTCCCAATCAAAATTAACAACCCCTGCAATTTAGTCTTATTACAATTTCAAGCTT 665
Qy 759 TTTACAATCTAGCTGGTGGAA 779
Db 666 TAAGGATTTACTGGGAGTA 686

RESULT 3
AZ538746/c

LOCUS AZ538746 862 bp DNA linear GSS 14-NOV-2000
DEFINITION ENTDM6STF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

ACCESSION AZ538746
VERSION AZ538746
KEYWORDS AZ538746.1 GI:11143976
SOURCE GSS.
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 862)
AUTHORS Loftus,B., Van Aken,S. and Fraser,C.
TITLE Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 36
High quality sequence stop: 832.
Location/Qualifiers
FEATURES
source
1. .862
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."

ORIGIN
Query Match 1.4%; Score 46.2; DB 8; Length 862;
Best Local Similarity 52.8%; Pred. No. 0.17;
Matches 123; Conservative 0; Mismatches 108; Indels 2; Gaps 1;
Qy 1449 GGAATGTCACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAC 1508
Db 771 GGAATAACTACCAAAATGGAATAATATTTTATTAAT--GGACAAATAAATCAATA 714
Qy 1509 TAGCAAAAGTCAATGTCAAACCTAGCAGCATCTGCTCTCATTAACCTATATCGTTTGA 1568
Db 713 GTGTAATATTAGAAATTAATCAAAAATAACATATGGAATAATTTATCTTATGTTTAA 654
Qy 1569 CTATCATATCTCTTTGTTGGTATATCTAGCCGTGATTCAGCATGCTACCTAATGTACA 1628
Db 653 CAATATTAAATTATTATCTTAATTACAATTTGGAATGTTTATTTGTAATATACAGAAATTATA 594
Qy 1629 AGCAAAAGGCCACAAAAACCTTATTATGGCTTGGGAATAAATCTCTAGAT 1681
Db 593 ATAAAGAAAGAAAGATAAATTAAGAGTGGATTAAATTAATCAATTATAT 541

RESULT 4
AZ541254/c
LOCUS

DEFINITION ENTFA11TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

ACCESSION AZ541254
VERSION AZ541254.1 GI:11148809
KEYWORDS GSS.
SOURCE Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 886)
AUTHORS Loftus,B., Van Aken,S. and Fraser,C.
TITLE Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 27
High quality sequence stop: 842.
Location/Qualifiers
FEATURES
source
1. .886
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."

ORIGIN
Query Match 1.4%; Score 46.2; DB 8; Length 886;
Best Local Similarity 52.8%; Pred. No. 0.17;
Matches 123; Conservative 0; Mismatches 108; Indels 2; Gaps 1;
Qy 1449 GGAATGTCACAACTCGATCAGTAATGCTTTGAATAAGTTAGAGAAAGCAACAGAAAC 1508
Db 568 GGAATAACTACCAAAATGGAATAATATTTTATTAAT--GGACAAATAAATCAATA 511
Qy 1509 TAGCAAAAGTCAATGTCAAACCTAGCAGCATCTGCTCTCATTAACCTATATCGTTTGA 1568
Db 510 GTGTAATATTAGAAATTAATCAAAAATAACATATGGAATAATTTATCTTATGTTTAA 451
Qy 1569 CTATCATATCTCTTTGTTGGTATATCTAGCCGTGATTCAGCATGCTACCTAATGTACA 1628
Db 450 CAATATTAAATTATTATCTTAATTACAATTTGGAATGTTTATTTGTAATATACAGAAATTATA 391
Qy 1629 AGCAAAAGGCCACAAAAACCTTATTATGGCTTGGGAATAAATCTCTAGAT 1681
Db 390 ATAAAGAAAGAAAGATAAATTAAGAGTGGATTAAATTAATCAATTATAT 338

RESULT 5
AY032979/c
LOCUS
DEFINITION AY032979 upregulated by angiotensin II in mesangial cells Homo

sapiens cDNA clone Angrgm-52f, mRNA sequence.

ACCESSION

AY032979

VERSION

AY032979.1 GI:20429781

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 406)

REFERENCE

Zhou, A., Zhang, H. and Wang, H.

AUTHORS

Cloning and identification of a novel gene up-regulated in human

TITLE

mesangial cells stimulated by angiotensin II

JOURNAL

Unpublished (2002)

COMMENT

Contact: Zhou, A., Zhang, H. and Wang, H.

Peking University

Institute of Nephrology

No. 8, Xishiku St., Beijing, 100034, P. R. China.

FEATURES

Location/Qualifiers

source

1..406

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="Angrgm-52f"

/clone_lib="upregulated by angiotensin II in mesangial cells"

ORIGIN

Query Match 1.3%; Score 43.6; DB 2; Length 406;

Best Local Similarity 47.2%; Pred. No. 0.74;

Matches 133; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 401 GGCGCCATTATTCGGGTGGCTCTTGGGGTTCGCACTGCCGACAAATAACAGCGGCC 460

DB 282 GGGCGGTTCATCGGTGGAGTTGCAATAGGGGTGGCGACTTCAGCGCAGATTACAGCGGC 223

QY 461 GCAGCTCTGATACAAGCCAAACAAATGCTGCCAACATCTCCGACTTAAAGAGAGCATT 520

DB 222 GTTGCTCTTCACAACTCCATTCAGAATGCAATGCTATTGTGACACTCAAGATTCTATC 163

QY 521 GCAGCAACCAATAGGCTGTGATGAGGTCACTGACGGATATTCGCAACTAGCAGTGGCA 580

DB 162 AGGCAGCTAACCAAGCAATACAGAATTACAAACAGCTATGTCTACCACTGTGCTGTG 103

QY 581 GTTGGGAAGATGCGAGCTTTGTTAATGACCAATTTAATAAACAGCTCAGGAATTAGAC 640

DB 102 TTAATGCTCTCCAGGACCCAGATAAATAACAGTTGGCCCCAGCTATAAATTTCTAGGA 43

QY 641 TGCATCAAAATTGCACAGCAAGTTGGGTAGAGCTCAACCTG 682

DB 42 TGCCAGGTGGTTGCTAATACACTAGGTCTAAATTAACACAG 1

RESULT 6

AW329422

LOCUS

AW329422 386 bp mRNA linear EST 01-MAY-2000

DEFINITION

N200657e rootphos(-) Medicago truncatula cDNA clone MHRP-19H9, mRNA

ACCESSION

AW329422

VERSION

AW329422.1 GI:6800017

KEYWORDS

EST.

SOURCE

Medicago truncatula (barrel medic)

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 386)

Harrison, M.J., Liu, J., Harris, A.R., Scott, A.D., Gonzales, R.A.,

Gonzales, M.B., and Ellis, L.

ESTs from phosphate starved roots

Unpublished (1999)

Contact: Harrison M.J.

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73401

Tel: 580-223-5810

Fax: 580-221-7380

Email: mjharrison@noble.org

Date: 1/23/00; updated to the Database of Expressed Sequence Tags

(dbEST) on 04/27/00; More information is available at

'http://chrysis.tamu.edu/medicago'.

Seq primer: T3.

FEATURES

source

1..386

/organism="Medicago truncatula"

/mol_type="mRNA"

/cultivar="Jemalong, line A17"

/db_xref="taxon:3880"

/clone="MHRP-19H9"

/tissue_type="roots"

/dev_stage="phosphate starved"

/clone_lib="rootphos(-)"

/note="Vector: pBluescript SK -; Site 1: EcoRI; Site 2:

XhoI; At the trifoliolate stage, M. truncatula plants were

transplanted to phosphate-free sand and grown for a

further 30 days. During this 30 day period, they were

fertilized twice weekly with 1/2 Hoaglands solution

containing only 20uM potassium phosphate. RNA was prepared

from the roots. cDNA was prepared from polyA+ enriched

RNA. The cDNA was directionally ligated into the Unizap XR

vector from Stratagene and packaged using Gigapack III

Gold packaging extracts. Plasmids containing cDNA inserts

were excised from the recombinant lambda-Zap phage using

Ex-assist helper phage and propagated in SOLR cells."

ORIGIN

Query Match 1.3%; Score 43.2; DB 2; Length 386;

Best Local Similarity 50.0%; Pred. No. 0.96;

Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 1394 ATACAAGATTCTCAAGTAATAATAACAGGCAATCTTGATATCTCAACTGAGCTGGGAAT 1453

DB 81 ATAGCATAAACCTAGCAATTAATGGTGAATTAATCTACACGCTGGTGTAGGT 140

QY 1454 GTCAACAACCTCGATCAGTAATGCTTTGAATTAAGTTAGAGAAAGCAACAGAAAAGTAC 1513

DB 141 GTHAATCATCTGCTGCAAGAACAAATGAATGGTTCTCGAAGAGAGACAGAAAGAGAG 200

QY 1514 AAGTCAATGTCAACTAGCAGCATCTGCTCTCTATTACCTATATCGTTTGACTATC 1573

DB 201 AGATCAAGTTTGTAATATATCTTCTTAACGGAAGCTTTGTAAGTTTGTGGTAAATC 260

QY 1574 ATATCTCTGTTTGTGATATCTAGCTGATCTTA 1609

DB 261 ATACGTTTGAGTTTAGTTGCTTTTGGACTTTA 296

RESULT 7

AL380807

LOCUS

AL380807 494 bp mRNA linear EST 03-AUG-2000

DEFINITION

McBB54F09R1 MtBB Medicago truncatula cDNA clone McBB54F09 T7, mRNA

ACCESSION

AL380807

VERSION

AL380807.1 GI:9680559

KEYWORDS

EST.

SOURCE

Medicago truncatula (barrel medic)

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 494)

Journet, E.P., Crespeau, H., van Tuinen, D., Gouzy, J., Jaillon, O.,

Niebel, A., Carreau, V., Chatagnier, O., Kahn, D.,

Gianinazzi-Pearson, V. and Gamas, P.

Medicago truncatula ESTs from Sinorhizobium meliloti-induced root

using Tetraodon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)
 20296633
 MEDLINE
 PUBMED
 10835645

2
 AUTHORS
 Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
 Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
 Saurin,W., Bernot,A. and Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Genome Res. 10 (7), 939-949 (2000)

JOURNAL
 MEDLINE
 PUBMED
 10899143

REFERENCE
 3 (bases 1 to 1022)
 Genoscope.
 Direct Submission
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : secrete@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES
 source
 1. .1022
 Location/Qualifiers
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="049L07"
 /clone_lib="G"
 /note="Genoscope sequence ID : COBG049CF048P1-end :
 PUC-Ori"

ORIGIN
 Query Match 1.3%; Score 42.6; DB 9; Length 1022;
 Best Local Similarity 49.3%; Pred. No. 2.1;
 Matches 111; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
 QY 1360 GGAATTCGATGTAATCTATCAGAGAATATCTCAATACAGATTCCTCAAGTAATAAATAC 1419
 Db GTTATTTAGATTACCGTACCAAAATTTCTATATGCTAAATGGCAAGTATATGAAGAAG 778
 QY 1420 AGCAATCTTGATATCTCAATCGATGTTGGGAATGTCAACAATCTCGATCAAGTAATGCTTT 1479
 Db GAGAAATCTGTATTCTCTCCAAAGAGTCAGAAGTTTGCATACACTATTACTATGCGCTTT 718
 QY 1480 GAATAAGTTAGAAAGCAACAGAACTAGACAAAGTCAATGTCAAACTGACTAGACAC 1539
 Db AAACAATTTGGGGAAGCCCAAGTGATTATGTCACTACCTTGGAAATATTATTGAAAGTCTC 658
 QY 1540 ATCTGCTCTCATTACCTATATCGTTTGGACTATCATATCTCTGTT 1584
 Db TGATAGGTTTATTAAACAATGTTGTTCAATCTTTTCAACAATATTAT 613

RESULT 10
 CD081007
 LOCUS
 DEFINITION
 MA3-9999U-M317-D07-U.G MA3-0001 Schistosoma mansoni cDNA clone
 MA3-9999U-M317-D07.G, mRNA sequence.
 CD081007
 CD081007.1 GI:34632000
 EST.
 Schistosoma mansoni
 Schistosoma mansoni
 ORGANISM
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 507)
 Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
 Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
 Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
 Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
 Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,

Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
 Sa,R.G., Stukart,G., Soares,M.B., Gargioni,C., Kawano,I.,
 Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
 Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
 Transcriptome analysis of the acoelomate human parasite Schistosoma
 mansoni
 Nat. Genet. 35 (2), 148-157 (2003)
 22879926
 MEDLINE
 PUBMED
 12973350

COMMENT
 Contact: Dr. Sergio Verjovski-Almeida
 Departamento de Bioquímica
 Instituto de Química - Universidade de São Paulo
 Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,
 Brasil
 Tel: +55-11-3091-2173
 Fax: +55-11-3091-2186
 Email: verjo@iq.usp.br
 This sequence was derived from the FAPESP Schistosoma mansoni EST
 Genome Project. All sequences in the project were assembled and
 annotated. This entry and all the assembled sequences can be seen
 in the following URL http://bioinfo.iq.usp.br/schisto/
 Plate: MA3-9999U-M317 row: 7 column: D.

FEATURES
 source
 1. .507
 Location/Qualifiers
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="MA3-9999U-M317-D07.G"
 /sex="mixed pool"
 /dev_stage="adult"
 /lab_host="Mus musculus"
 /clone_lib="MA3-0001"

ORIGIN
 Query Match 1.3%; Score 42.4; DB 6; Length 507;
 Best Local Similarity 49.4%; Pred. No. 1.8;
 Matches 88; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
 QY 1481 AATAAGTTAGAGAAAGCAAGAACTAGACAAAGTCAATGCTCAAACTGACTAGACACA 1540
 Db AACAAGTTCCCAATACACACACACACACACACCGTTATTAAAGCGTTACTAGCTAA 189
 QY 1541 TCTGCTCTCATTAACCTATATCGTTTGGACTATCATATCTCTTGTGTTGTTACTTAGC 1600
 Db ACCGTGTCATACAGTTTATTCCTTGAATAATATTTCAGACATTTAATCGTCACITGGA 249
 QY 1601 CTGATTTCTAGCATGCTACCTAATGTACAGCAAGCGCACACAAAACCTTATTAT 1658
 Db TCCAATCTTCATGTTTACCGGATTTTACCAGCGATNNNNNNNNNNNAGCAATAAT 307

RESULT 11
 BH183366/c
 LOCUS
 DEFINITION
 023_G 14-21 SmbAC1 Schistosoma mansoni genomic clone 023G14 5',
 genomic survey sequence.
 BH183366
 BH183366.1 GI:16288520
 GSS.
 Schistosoma mansoni
 Schistosoma mansoni
 ORGANISM
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 816)
 Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,
 Williams,D.U., Johnston,D., Loverde,P.T. and Le Paslier,D.
 Construction and characterization of a Schistosoma mansoni
 bacterial artificial chromosome library
 Genomics 65 (2), 87-94 (2000)
 20247247
 MEDLINE
 PUBMED
 10783255

COMMENT
 Other_GSSs: 023_G 14-rev
 Contact: Pierce_RJ

This Page Blank (uspto)